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OM protein - protein search, using sw model

Run on: August 30, 2004, 17:00:32 ; Search time 38 seconds
(without alignments)
192.383 Million cell updates/sec

Title: 07330446.PEP

Perfect score: 405

Sequence: 1 qpdaipvtccynftrkri.....qkvwgdmhldkqtgtpkt 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	99	2 A60299	monocyte chemoattr
2	337	83.2	99	2 JC2136	monocyte chemoattr
3	315	77.8	99	1 A39296	monocyte chemoattr
4	315	77.8	99	2 JC2336	monocyte chemoattr
5	314	77.5	125	2 I46857	monocyte chemoattr
6	288	71.1	72	2 A55984	monocyte chemoattr
7	287	70.9	109	2 A54678	monocyte chemoattr
8	270	66.7	97	2 JC4912	ectaxin precursor
9	268	66.2	99	2 JC5295	monocyte chemoattr
10	261	64.4	99	2 JC2417	monocyte chemoattr
11	252	62.2	148	1 A30209	PDGF-inducible JE
12	241	59.5	148	1 S07723	immediate-early se
13	236	58.3	120	2 I48147	monocyte chemoattr
14	214	52.8	96	2 I48099	ectaxin precursor
15	207	51.1	96	2 JC2478	ectaxin precursor
16	200	49.4	97	2 A46093	monocytic cytokine
17	145.5	35.9	93	2 B35673	LD78-beta protein
18	142.5	35.2	92	2 A30574	macrophage inflamm
19	135.5	33.5	92	1 A31767	macrophage inflamm
20	133.5	33.0	92	2 I46730	immune activation
21	127.5	31.5	92	2 C30552	macrophage inflamm
22	123	30.4	92	2 I52322	macrophage inflamm
23	119	29.4	92	2 A32393	macrophage inflamm
24	108.5	26.8	91	1 A46539	monocyte chemoattr
25	106	26.2	120	2 JE0177	lymphocyte and mon
26	105.5	26.0	91	1 A28815	monocyte chemoattr
27	99.5	24.6	96	2 A37236	I-309 protein precu
28	99.5	24.6	114	2 ETHUL	lymphotactin precu
29	98	24.2	50	2 C60407	monocyte adherence

ALIGNMENTS

RESULT 1

A60299

monocyte chemoattractant protein 1 precursor - human

N/Alternate names: GDCP-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1; mon

N/Contains: glioma-derived chemotactic factor 2 (GDCF-2)

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1993 #sequence, revision 20-Feb-1993 #text change 16-Jul-1999

C/Accession: A35474; A33476; S03339; I51841; A60299; A32300; A32396; A34561; I57488; JCI:1

R:SHYV, Y.J.; Li, Y.S.; Kolattukudy, P.E.

Biochem. Biophys. Res. Commun. 169, 346-351, (1990)

A/Title: Structure of human monocyte chemoattractant protein gene and its regulation by TPA.

A/Reference number: A35474; MUID:90290466; PMID:2357211

A/Accession: A35474

A/Molecule type: DNA

A/Residues: 1-99 <SHY>

A/Cross-references: GB:M37719; NID:G187447; PIDN:AAA18102.1; PID:G487124

R:Rollins, B.J.; Stier, P.; Ernest, T.; Wong, G.G.

Mol. Cell. Biol. 9, 4687-4695, (1989)

A/Title: The human homolog of the c-fos gene encodes a monocyte secretory protein.

A/Reference number: A33476; MUID:90097880; PMID:2513477

A/Accession: A33476

A/Molecule type: mRNA

A/Residues: 1-99 <ROI>

A/Cross-references: GB:M30816; GB:M31625; GB:M31626; NID:G188701; PIDN:AAA36330.1; PID:G

R:Yoshimura, T.; Fukui, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, E.J.

FEBS Lett. 244, 487-493, (1989)

A/Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, exp

A/Reference number: S03339; MUID:89153605; PMID:2465924

A/Accession: S03339

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-99 <YOS>

A/Cross-references: GB:X14768; NID:G34513; PIDN:CAA32876.1; PID:G34514

A/Experimental source: glioma cell line U-105MG

R:Yoshimura, T.; Leonard, E.J.

Adv. Exp. Med. Biol. 305, 47-56, (1991)

A/Title: Human monocyte chemoattractant protein-1 (MCP-1).

A/Reference number: I51841; MUID:92095166; PMID:1661560

A/Accession: I51841

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-99 <YOS>

A/Cross-references: GB:S71513; NID:G240867; PIDN:AAB20651.1; PID:G240868

R:Buttazzi, B.; Colotta, F.; Sica, A.; Nobili, N.; Mantovani, A.

Int. J. Cancer 45, 795-797, (1990)

A/Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic f

-1/MCAF).

A/Reference number: A60299; MUID:90216082; PMID:2182547

A/Accession: A60299

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

30 94 23.2 103 2 A53096 interleukin-8 prec
31 93.5 23.1 92 2 S24236 TCA3 protein - mou
32 91.5 22.6 114 1 BTMSL lymphotactin precu
33 83 20.5 101 2 I48148 Neutrophil attract
34 79 19.5 101 2 S42496 interleukin-8 prec
35 79 19.5 101 2 I46871 interleukin-8 - ra
36 75 18.5 95 2 JN0841 interleukin-8 - do
37 73.5 18.1 116 2 I49555 gene C10 protein -
38 70 17.3 99 2 A37034 interleukin-8 prec
39 66 16.3 2867 2 AG3481 cellobiose-phospho
40 65.5 16.2 143 2 S76162 hypothetical prote
41 65 16.0 282 2 S44825 F54F2.8 protein -
42 64.5 15.9 363 2 T26700 hypothetical prote
43 64 15.8 1019 2 E90097 hypothetical prote
44 64 15.8 1076 2 F96831 hypothetical prote
45 62.5 15.4 853 2 AB2020 hypothetical prote

A;Residues: 1-99 <BOT>
R;Furtani, Y.; Nomura, H.; Notake, M.; Oyama, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.
Biochem. Biophys. Res. Commun. 159, 249-255, 1989
A;Title: Cloning and sequencing of the cDNA for human monocyte chemoattractant and activation
A;Reference number: A32300; MUID:89165862; PMID:2923622
A;Accession: A32300
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-99 <FUR>
A;Cross-references: GB:M24545; NID:G187434; PIDN:AAA18164.1; PID:G307163
R;Robinson, E.A.; Yoshimura, T.; Leonard, E.J.; Tanaka, S.; Griffin, P.R.; Shabanowitz,
Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1854, 1989
A;Title: Complete amino acid sequence of a human monocyte chemoattractant, a putative me
A;Reference number: A32396; MUID:89184525; PMID:2648385
A;Accession: A32396
A;Molecule type: protein
A;Residues: 'X', 25-99 <ROB>
R;Deacock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.
Biochem. Biophys. Res. Commun. 157, 904-909, 1990
A;Title: Identification of the monocyte chemoattractant protein from human osteosarcoma cell
A;Reference number: A34561; MUID:90211336; PMID:2322826
A;Accession: A34561
A;Molecule type: protein
A;Residues: 29-33, 'XX', 36-52; 82-92 <DEC>
R;Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.
Mol. Cell. Biochem. 126, 61-69, 1993
A;Title: The expression of monocyte chemoattractant protein (MCP-1) in human vascular endoth
A;Reference number: I57488; MUID:94150478; PMID:8107690
A;Accession: I57488
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-99 <LTV>
A;Cross-references: GB:S69738; NID:9545464; PIDN:AA829926.1; PID:G545465
R;Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.
Chinese J. Microbiol. Immunol. 14, 29-32, 1994
A;Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1 (MCP
A;Reference number: JCI1096
A;Accession: JCI1096
A;Molecule type: mRNA
A;Residues: 24-28, 'Q', 30-39 <VEQ>
C;Genetics:
A;Gene: GDB:SCYA2
A;Cross-references: GDB:123279; OMIM:158105
A;Map position: 17q11.2-17q12
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation; pyroglutamic acid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein 1 #status experimental <MAT>
F;24-99/Product: monocyte chemoattractant protein 1, short form #status experimental <MA
F;24/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimen
F;37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5e-39;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 2
JC2136
monocyte chemoattractant protein-1 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
C;Accession: J57498
R;Hosang, K.; Knoke, I.; Klaidiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994

A;Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysis
A;Reference number: JC2136; MUID:94183284; PMID:7510962
A;Accession: JC2136
A;Molecule type: mRNA
A;Residues: 1-99 <HOS>
A;Cross-references: GB:Z48479; NID:G683716; PIDN:CAA88370.1; PID:G683717
R;Zach, O.
submitted to the EMBL Data Library, July 1994
A;Reference number: S57497
A;Accession: S57498
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-99 <ZAC>
A;Cross-references: EMBL:X79416; NID:9872312; PIDN:CAAS5945.1; PID:9872313
C;Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.2%; Score 337; DB 2; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPKT 75
DB 84 QDSMDHLDKQTQTPKT 98

RESULT 3
A32396
monocyte chemoattractant protein 1 precursor - bovine
N;Alternate names: monocyte chemoattractant factor 1; seminal plasma protein P6
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A32296; B32296
R;Wempe, F.; Henschen, A.; Scheit, K.H.
DNA Cell Biol. 10, 671-679, 1991
A;Title: Gene expression and cDNA cloning identified a major basic protein constituent of
A;Reference number: A32296; MUID:92096117; PMID:1721821
A;Accession: A32296
A;Molecule type: mRNA
A;Residues: 1-99 <WEM>
A;Cross-references: GB:M84602; GB:M85264; NID:G163394; PIDN:AAA30651.1; PID:G163395
A;Accession: B32296
A;Molecule type: protein
A;Residues: 50-68, 'X', 70-74, 'X', 76 <WE2>
A;Experimental source: seminal vesicle
C;Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein 1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 77.8%; Score 315; DB 1; Length 99;
Best Local Similarity 73.3%; Pred. No. 5.3e-29;
Matches 55; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPKT 75
DB 84 QDSMDHLDKQTQTPKT 98

RESULT 4
JC22336

monocyte chemoattractant protein-1 - bovine
C:Species: Bos primigenius indicus (zebu cattle)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-May-1996
C:Accession: J02336
R:Wempe, F.; Kuhlmann, J.K.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 202, 1272-1279, 1994
A:Title: Characterization of the bovine monocyte chemoattractant protein-1 gene.
A:Reference number: J02336; MUID:94338337; PMID:8060303
A:Accession: J02336
A:Molecule type: Protein
A:Residues: 1-99 <MEM>
C:Genetics:
A:Gene: MCP-1
A:Introns: 26/1; 65/2
C:Superfamily: macrophage inflammatory protein

Query Match 77.8%; Score 315; DB 2; Length 99;
Best Local Similarity 73.3%; Pred. No. 5.3e-29;
Matches 55; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 QPDANAPVTCYNTNKRISQVRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDANISQVACCTFNKSIQVRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPK 75
DB 84 QDSINYLNKKNQTPK 98

RESULT 5
I46857
monocyte chemoattractant protein-1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46857
R:Yoshimura, T.; Yuhki, N.
J. Immunol. 146, 3483-3488, 1991
A:Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein
A:Reference number: I46857; MUID:91225489; PMID:2026877
A:Accession: I46857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-125 <YOS>
A:Cross-references: GB:M57440; NID:gl65469; PIDN:AAA31386.1; PID:gl65470
C:Superfamily: macrophage inflammatory protein

Query Match 77.5%; Score 314; DB 2; Length 125;
Best Local Similarity 75.0%; Pred. No. 8.8e-29;
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 QPDANAPVTCYNTNKRISQVRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDANSPVTCCTFTNKTISVKRLMSYRRITSSKCPKEAVIFMTKLAKGICADPKQKW 83

QY 61 QDSMDHLDKQTQTPK 76
DB 84 QDAIANLDRKNQTPK 99

RESULT 6
A55984
monocyte chemoattractant protein bo-MCP-1b - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-May-1997
C:Accession: A55984
R:Proost, P.; Wuyts, A.; Lenaerts, J.P.; Van Damme, J.
Biochemistry 33, 13406-13412, 1994
A:Title: Purification, sequence analysis, and biological characterization of a second bo
A:Reference number: A55984; MUID:95034774; PMID:7947749
A:Accession: A55984
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-72 <PRO>

C:Superfamily: macrophage inflammatory protein

Query Match 71.1%; Score 288; DB 2; Length 72;
Best Local Similarity 74.0%; Pred. No. 4.9e-26;
Matches 54; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

QY 3 DAINAPVTCYNTNKRISQVRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62
DB 1 DAINSPVTCCTFTNKTISVKRLMSYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 58

QY 63 SMDHLDKQTQTPK 75
DB 59 SISHLDKKNQXPK 71

RESULT 7
A54678
monocyte chemotactic protein 3 precursor - human
N:Alternate names: monocyte chemoattractant protein MCP-3
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C:Accession: A54678; J01478; S32222
R:Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.
Genomics 21, 403-408, 1994
A:Title: The human MCP-3 gene (SCVA7): cloning, sequence analysis, and assignment to the
A:Reference number: A54678; MUID:94375065; PMID:7916328
A:Accession: A54678
A:Molecule type: DNA
A:Residues: 1-109 <OPD>
A:Cross-references: GB:X72309
R:Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
A:Title: Human monocyte chemoattractant protein-3 (MCP-3): Molecular cloning of the cDNA and
A:Reference number: J01478; MUID:93213290; PMID:8461011
A:Accession: J01478
A:Molecule type: mRNA
A:Residues: 1-109 <OP2>
A:Cross-references: GB:X72308; GB:S57464; NID:g328270; PIDN:CAA51055.1; PID:g313708
R:Minty, A.; Chalon, P.; Guillemot, J.C.; Kagnad, M.; Liauzon, P.; Magazin, M.; Miloux,
submitted to the EMBL Data Library, March 1993
A:Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattract
A:Reference number: S32222
A:Accession: S32222
A:Molecule type: mRNA
A:Residues: 1-109 <MIN>
A:Cross-references: EMBL:X71087; NID:g288396; PIDN:CAA50405.1; PID:g288397
C:Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m
C:Genetics:
A:Gene: GDB:SCVA7; SCVA6; MCP-3
A:Cross-references: GDB:I38473; OMIM:158106
A:Map position: 17q11-17q12
A:Introns: 36/1; 75/2
C:Superfamily: macrophage inflammatory protein
C:Keywords: cytokine; glycoprotein; inflammation
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>
F:39/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.9%; Score 287; DB 2; Length 109;
Best Local Similarity 72.0%; Pred. No. 9.6e-26;
Matches 54; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 QPDANAPVTCYNTNKRISQVRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 34 QPVGINSTTCYRFINKIPKQRLSVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 93

QY 61 QDSMDHLDKQTQTPK 75
DB 94 QDFMKHLDDKKTQTPK 108

RESULT 8
JC4912

N:Alternate names: monocyte chemoattractant protein-1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S07723; JN0128
R:Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res. 18, 23-34, 1990
A:Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential for transcriptional activation of the rat JE gene
A:Reference number: S07723; MUID:90174947; PMID:2106664
A:Accession: S07723
A:Molecule type: DNA
A:Residues: 1-148 <TIM>
A:Cross-references: EMBL:X17053; NID:g55530; PIDN:CAA34901.1; PID:g55531
R:Yoshimura, T.; Takeya, M.; Takahashi, K.
Biochem. Biophys. Res. Commun. 174, 504-509, 1991
A:Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its expression in macrophages
A:Reference number: JN0128; MUID:91128376; PMID:1704226
A:Accession: JN0128
A:Molecule type: mRNA
A:Residues: 1-148 <YOS>
A:Cross-references: GB:M57441; NID:g205333; PIDN:AAA63496.1; PID:g205334
A:Experimental source: spleen cells
A:Note: the authors translated the codon GAA for residue 62 as Lys and GGT for residue 63
C:Genetics: 26/1; 65/2
A:Insertions: 26/1; 65/2
C:Superfamily: macrophage inflammatory protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>

Query Match 59.5%; Score 241; DB 1; Length 148;
Best Local Similarity 55.3%; Pred. No. 2.4e-20;
Matches 42; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 24 QPDVAVNAPLTCYVSFTGKMPMSRLNRYKRITSSRCPEAVVFTVKLKEICADPNKEWV 83

QY 61 QDSMDHLDKQTQPKT 76
Db 84 QKYIRKLDQNVASET 99

RESULT 13
I48147
monocyte chemoattractant protein-1 - guinea pig
C:Species: Cavia porcellus (Guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I48147
R:Yoshimura, T.
J. Immunol. 150, 5025-5032, 1993
A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of the complementary DNA in COS cells
A:Reference number: I48147; MUID:93267104; PMID:8496603
A:Accession: I48147
A:Molecule type: mRNA
A:Residues: 1-120 <RES>
A:Cross-references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
C:Genetics:
A:Gene: MCP-1
C:Superfamily: macrophage inflammatory protein

Query Match 58.3%; Score 236; DB 2; Length 120;
Best Local Similarity 59.7%; Pred. No. 7.4e-20;
Matches 43; Conservative 14; Mismatches 13; Indels 2; Gaps 2;

QY 1 QPDAINAPVTCYNNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 24 QPDGVNTPF-TCCYTF-NKQPLKRVKGYRITSSRCPEAVIFRTLNKEVCADPTQKWV 81

QY 61 QDSMDHLDKQTO 72
Db 82 QDYIAKUCQRIQ 93

RESULT 14
I48099
eotaxin precursor - guinea pig
C:Species: Cavia porcellus (Guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I48099
R:Rothenberg, M.E.; Luster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
J. Exp. Med. 181, 1211-1216, 1995
A:Title: Constitutive and allergen-induced expression of eotaxin mRNA in the guinea pig
A:Reference number: I48099; MUID:95173589; PMID:7869037
A:Accession: I48099
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <RES>
A:Cross-references: EMBL:U18941; NID:g687655; PIDN:AAC52180.1; PID:g687656
C:Superfamily: macrophage inflammatory protein

Query Match 52.8%; Score 214; DB 2; Length 96;
Best Local Similarity 57.4%; Pred. No. 2e-17;
Matches 39; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 8 PVTCCYNNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWVDSMDHL 67
Db 28 PSACCFRVTNKKISFQRLKSYKIITSSKCPQTAIVFEIKPDKMICADPKKKWVQDAKKYL 87

QY 68 DKQQTQPK 75
Db 88 DQISQTTK 95

RESULT 15
JC2478
eotaxin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C:Accession: JC2478
R:Jose, P.J.; Adcock, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.C.; Williams, B.
Biochem. Biophys. Res. Commun. 205, 788-794, 1994
A:Title: Eotaxin: Cloning of an eosinophil chemoattractant cytokine and increased mRNA expression in allergic rhinitis
A:Reference number: JC2478; MUID:95091818; PMID:7999113
A:Accession: JC2478
A:Molecule type: mRNA
A:Residues: 1-96 <YOS>
A:Cross-references: EMBL:X77603; NID:g602551; PIDN:CAA54698.1; PID:g602552
C:Comment: This protein is identified as a potent eosinophil chemoattractant.
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-96/Product: eotaxin #status predicted <MAT>
F:93/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match 51.1%; Score 207; DB 2; Length 96;
Best Local Similarity 55.9%; Pred. No. 1.3e-16;
Matches 38; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 8 PVTCCYNNFTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWVDSMDHL 67
Db 28 PSACCFRVTNKKISFQRLKSYKIITSSKCPQTAIVFEIKPDKMICADPKKKWVQDAKKYL 87

QY 68 DKQQTQPK 75
Db 88 GQISQTTK 95

Search completed: August 30, 2004, 17:08:02
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 17:02:47 ; Search time 32 Seconds
(without alignments)
122.612 Million cell updates/sec

Title: 07330446.PEP

Perfect score: 405

Sequence: 1 cpdaiapvccynftnrki.....qkwvqdsmdhldkqtqpk 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/2/iaa/PCUTUS_COMB.pep:*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	76	2	US-08-716-188-2
2	405	100.0	76	2	US-08-615-232A-5
3	405	100.0	76	3	US-08-470-323-5
4	405	100.0	76	4	US-09-195-457-5
5	405	100.0	76	4	US-09-291-038-5
6	405	100.0	78	1	US-08-330-163-12
7	405	100.0	78	1	US-08-482-111-12
8	405	100.0	99	1	US-08-127-499A-35
9	405	100.0	99	1	US-08-482-847-35
10	405	100.0	99	1	US-08-347-492B-8
11	405	100.0	99	1	US-08-480-449-19
12	405	100.0	99	2	US-08-479-126B-5
13	405	100.0	99	2	US-08-421-144A-5
14	405	100.0	99	2	US-08-726-830A-5
15	405	100.0	99	2	US-08-660-542-19
16	405	100.0	99	2	US-08-798-143-8
17	405	100.0	99	3	US-07-927-391-24
18	405	100.0	99	3	US-08-995-156A-5
19	405	100.0	99	3	US-09-044-856A-5
20	405	100.0	99	3	US-09-044-855A-5
21	405	100.0	99	4	US-08-679-493A-152
22	405	100.0	99	4	US-08-479-603-19
23	405	100.0	99	4	US-09-419-281-5
24	405	100.0	99	4	US-09-366-887A-10
25	405	100.0	99	4	US-08-339-107-19
26	405	100.0	99	4	US-09-545-894-5
27	405	100.0	99	5	PCT-US96-10087-5

28	405	100.0	99	6	5212073-2	Patent No. 5212073
29	400	98.8	76	1	US-07-956-862A-1	Sequence 1, Appli
30	400	98.8	76	1	US-08-250-958-1	Sequence 1, Appli
31	400	98.8	76	1	US-08-235-659-1	Sequence 1, Appli
32	400	98.8	78	5	PCT-US95-00605-1	Sequence 1, Appli
33	362	89.4	68	4	US-09-463-458A-30	Sequence 30, Appli
34	362	89.4	69	4	US-09-463-458A-31	Sequence 31, Appli
35	362	89.4	69	4	US-09-463-458A-32	Sequence 32, Appli
36	358	88.4	68	4	US-09-463-458A-9	Sequence 9, Appli
37	358	88.4	68	4	US-09-463-458A-26	Sequence 26, Appli
38	358	88.4	68	4	US-09-463-458A-29	Sequence 29, Appli
39	315	77.8	99	3	US-09-133-521-5	Sequence 5, Appli
40	287	70.9	76	3	US-08-613-822-19	Sequence 19, Appli
41	287	70.9	76	4	US-09-479-729B-19	Sequence 19, Appli
42	287	70.9	76	4	US-09-717-209-19	Sequence 19, Appli
43	287	70.9	99	1	US-08-460-449-18	Sequence 18, Appli
44	287	70.9	99	2	US-08-660-542-18	Sequence 18, Appli
45	287	70.9	99	3	US-08-613-822-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-716-188-2
; Sequence 2, Application US/08716188
; Patent No. 5908829
; GENERAL INFORMATION:
; APPLICANT: KELLY, RODNEY W
; TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF
; TITLE OF INVENTION: THE CERVIX
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/716,188
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00733
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9406463.1
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-188-2

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Handwritten: MSCP-1
Handwritten: contract + agent

Qy 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 2

US-06-615-232A-5
; Sequence 5, Application US/08615232A
; Patent No. 5993814
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESS: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 76 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-615-232A-5

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 3

US-08-470-323-5

; Sequence 5, Application US/08470323A
; Patent No. 6031080
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/08/470,323A
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: PCT/GB94/02006
; EARLIER FILING DATE: 1994-09-14
; EARLIER APPLICATION NUMBER: GB 9318984.3
; EARLIER FILING DATE: 1993-09-14
; EARLIER APPLICATION NUMBER: GB 94086902.2
; EARLIER FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-08-470-323-5

Query Match 100.0%; Score 405; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 4

US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. 6605702

; GENERAL INFORMATION:

; APPLICANT: WILLIAMS, TIMOTHY J.

; APPLICANT: JOSE, PETER J.

; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.

; APPLICANT: HSUAN, JOHN J.

; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE

; FILE REFERENCE: 550-33

; CURRENT APPLICATION NUMBER: US/09/195,457

; CURRENT FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/470,323

; PRIOR FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: PCT/GB94/02006

; PRIOR FILING DATE: 1994-09-14

; PRIOR APPLICATION NUMBER: GB 9318984.3

; PRIOR FILING DATE: 1993-09-14

; PRIOR APPLICATION NUMBER: GB 94086902.2

; PRIOR FILING DATE: 1994-04-29

; NUMBER OF SEQ ID NOS: 11

; SEQ ID NO 5

; LENGTH: 76

; TYPE: PRT

; ORGANISM: human

US-09-195-457-5

Query Match 100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,111
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fasse, J. Peter
/ REGISTRATION NUMBER: 32,983
/ REFERENCE/DOCKET NUMBER: 00231/083001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 78 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-482-111-12

Query Match 100.0%; Score 405; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 6.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 3 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

Qy 61 QDSMDHLDKQOTPKT 76
Db 63 QDSMDHLDKQOTPKT 78

RESULT 8
US-08-127-499A-35
; Sequence 35, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-127-499A-35

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLDKQOTPKT 76
Db 84 QDSMDHLDKQOTPKT 99

RESULT 9
US-08-482-847-35
; Sequence 35, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-482-847-35

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLDKQOTPKT 76
Db 84 QDSMDHLDKQOTPKT 99

Epitope

AB

RESULT 10
US-08-347-492B-8
; Sequence 8, Application US/08347492B
; Patent No. 5602008
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
; PRODUCTION AND USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,492B
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,241
; FILING DATE: 07-SEP-1994
; APPLICATION NUMBER: 08/320,011
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 487124
US-08-347-492B-8
Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99
RESULT 11
US-08-480-449-19
; Sequence 19, Application US/08480449
; Patent No. 5688927
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,449
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gase, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/32779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "Hu MCP-1"
US-08-480-449-19

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 12
US-08-479-126B-5
; Sequence 5, Application US/08479126B
; Patent No. 5866373
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SUTTON, GRANGER G III
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE
; TITLE OF INVENTION: CHEMOTACTIC PROTEIN-4 (AS AMENDED)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

DNA

A B

Data No. 2
done

APPLICATION NUMBER: US/08/479,126B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340001
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-126B-5

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTPTKT 76
Db 84 QDSMDHLDKQTPTKT 99

RESULT 13
US-08-421-144A-5
Sequence 5, Application US/08421144A
Patent No. 5874211
GENERAL INFORMATION:
APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144A
FILING DATE: 13-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0031 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTPTKT 76
Db 84 QDSMDHLDKQTPTKT 99

RESULT 14
US-08-726-830A-5
Sequence 5, Application US/08726830A
Patent No. 5880263
GENERAL INFORMATION:
APPLICANT: LI, HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: MONOCYTE CHEMOTACTIC PROTEIN-4
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,830A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/479,126
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-830A-5

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-421-144A-5

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

QY 61 QDSMDHLDKQTPTKT 76
Db 84 QDSMDHLDKQTPTKT 99

RESULT 14
US-08-726-830A-5
Sequence 5, Application US/08726830A
Patent No. 5880263
GENERAL INFORMATION:
APPLICANT: LI, HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: MONOCYTE CHEMOTACTIC PROTEIN-4
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,830A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/479,126
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-830A-5

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
Qy 61 QDSMDHLDKQTQTPKT 76
Db 84 QDSMDHLDKQTQTPKT 99

Db 84 QDSMDHLDKQTQTPKT 99
Search completed: August 30, 2004, 17:08:40
Job time : 35 secs

RESULT 15
US-08-660-542-19
; Sequence 19, Application US/08660542
; Patent No. 5932703
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,542
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,658
; FILING DATE: 16-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,620
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/33318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "Hu MCP-1"
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..76
; US-08-660-542-19

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCVNFNTRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
Qy 61 QDSMDHLDKQTQTPKT 76

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OM protein - protein search, using sw model

Run on: August 30, 2004, 16:51:56 ; Search time 122 Seconds

(without alignments)
176.013 Million cell updates/sec

Title: 07330446.PEP

Perfect score: 405

Sequence: 1 gpdaipavtcyynftnrki.....gkwvqsdmdldkgtptp 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	76	2	AAR28660 MCF. 3/20
2	405	100.0	76	2	AAR87680 Monocyte
3	405	100.0	76	3	AAY69030 Amino aci
4	405	100.0	76	5	AAQ20010 Human che
5	405	100.0	76	5	AAQ14143 Human MCP
6	405	100.0	76	5	AAQ53048 Human mon
7	405	100.0	76	7	ADC89673 Human mat
8	405	100.0	76	7	ADD14998 Human mon
9	405	100.0	76	7	AD808952 huMCP1 ch
10	405	100.0	76	7	AD806777 Human MCP
11	405	100.0	99	1	AAP95387 Human mon
12	405	100.0	99	2	AAR28663 MCF. 3/20
13	405	100.0	99	2	AAR73914 Human mon
14	405	100.0	99	2	AAR70800 Chemocattr
15	405	100.0	99	2	AAW40174 Macrophag
16	405	100.0	99	2	AAY26176 Monocyte
17	405	100.0	99	2	AAY48391 Human pro
18	405	100.0	99	3	AA515785 Human che
19	405	100.0	99	4	AA97914 Human mon
20	405	100.0	99	5	AAW52440 HIV_Nef1
21	405	100.0	99	5	AAU77179 Human sma
22	405	100.0	99	5	AB80901 Human MCP
23	405	100.0	99	5	ABP65214 Hypoxia-r
24	405	100.0	99	6	ABP96799 Human COP
25	405	100.0	99	7	ABU10502 Human MCP

26	405	100.0	99	7	ADC89670	Adc89670 Human MCP
27	405	100.0	99	8	ADE48100	Ade48100 Human mon
28	405	100.0	122	7	ADD14997	Add14997 Human mon
29	405	100.0	325	3	AAY69049	Aay69049 A chemoki
30	405	100.0	327	3	AAY69050	Aay69050 A chemoki
31	405	100.0	332	3	AAY69051	Aay69051 A chemoki
32	402	99.3	76	2	AAW40175	AAw40175 Macrophag
33	402	99.3	76	3	AA512818	AA512818 Human gli
34	401	99.0	77	7	ADC89671	Adc89671 Human MCP
35	401	99.0	99	2	AAR06398	Aar06398 Human MCP
36	400	98.8	76	1	AAP90292	Aap90292 Peptide f
37	400	98.8	76	2	AAW09374	AAw09374 Monocyte
38	400	98.8	76	2	AAW11131	AAw11131 Mature hu
39	400	98.8	77	2	AA868959	AA868959 Mature MC
40	397	98.0	76	2	AAR87676	Aar87676 (24-Arg)
41	397	98.0	76	2	AAR87677	Aar87677 (3-Ala) M
42	395	97.5	76	2	AAR87675	Aar87675 (28-Asp)
43	391	96.5	77	2	AAW14222	AAw14222 Chemokine
44	389	96.0	76	2	AAR53398	Aar53398 Sense MCP
45	389	96.0	77	7	ADC89672	Adc89672 Human MCP

ALIGNMENTS

RESULT 1

AAR28660
ID AAR28660 standard; protein; 76 AA.

XX AAR28660;

AC AC

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

XX MCF.

DE MCF.

XX Plasmid; monocyte chemotactic factor; MCF; translation; termination;

KW terminator; initiation; ribosome binding site; RBS; promoter; tryptophan;

KW repressor.

XX Synthetic.

OS Synthetic.

XX W09219737-Al.

XX 12-NOV-1992.

XX 27-APR-1992; 92WO-JP000550.

XX 09-MAY-1991; 91JP-00135950.

XX (DAIN) DAINIPPON PHARM CO LTD.

XX Yamagishi J, Matsuo N, Fukui T, Yamada M;

XX WPI; 1992-398864/48.

XX N-PSDB; AAQ30745, AAQ30746.

XX Prodn. of polypeptide(s) having monocyte-chemotactic activity - using

XX expression plasmids with E. coli elements and specific E.coli strains.

XX Claim 1; Page 48 + Page 36; 56pp; English.

XX An expression plasmid, pHM483, for producing MCF(76) consisting of 76

XX amino acids was constructed. The prod. can be used for e.g. treating

XX bacterial infectious diseases. (Updated on 25-MAR-2003 to correct FN

XX field.)

XX Sequence 76 AA;

XX Query Match 100.0%; Score 405; DB 2; Length 76;

XX Best Local Similarity 100.0%; Pred. No. 8.7e-43;

XX Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 2
 AAR87680
 ID AAR87680 standard; protein; 76 AA.
 AC AAR87680;
 XX
 XX 05-MAR-1996 (first entry)
 DT Monocyte chemotactic activating factor for use as wound remedy.
 DE Monocyte chemotactic activating factor; MCPAF; wound remedy.
 KW monocyte chemotactic activating factor; MCPAF; wound remedy.
 XX Homo sapiens.
 OS
 PN WO9507710-A1.
 XX 23-MAR-1995.
 XX 13-SEP-1994; 94WO-JP001512.
 XX 13-SEP-1993; 93JP-00227385.
 XX (TORA) TORAY IND INC.
 XX Matsuushima K, Naruto M;
 XX WPI; 1995-131181/17.
 XX Wound treatment using monocyte chemotactic factor - has potent
 PT therapeutic effect on skin wounds and ulcers.
 PS Disclosure; Page 12; 22pp; Japanese.
 XX The invention relates to a new remedy for curing wounds which, instead of
 CC comprising a growth factor, comprises a monocyte chemotactic activating
 CC factor (MCAF) or its variants or derivatives. The factor has potent
 CC effect on skin wounds and ulcers. The present sequence is human MCAF, the
 CC activity of which is exemplified as the new remedy

QY 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 3
 AAY69030
 ID AAY69030 standard; protein; 76 AA.
 AC AAY69030;
 XX
 XX 30-MAY-2000 (first entry)
 DT Amino acid sequence of chemokine receptor ligand MCP-1.
 DE Antiarteriosclerotic; dermatological; anti-inflammatory; antiarthritic; antirheumatic;
 XX anti-allergic;

KW Chemokine receptor; ligand; inflammatory response; immune effector cell;
 KW secondary tissue damage; central nervous system injury; MCP-1;
 KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
 KW inflammatory eye disease; inflammatory bowel disease;
 KW inflammatory joint disease; inflammatory kidney; renal disease;
 KW inflammatory lung disease; inflammatory nasal disease;
 KW inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
 XX Homo sapiens.
 OS
 PN WO200004926-A2.
 XX 03-FEB-2000.
 XX 21-JUL-1999; 99WO-CA000659.
 XX 22-JUL-1998; 98US-00120523.
 XX (OSPR-) OSPREY PHARM LTD.
 XX McDonald JR, Coggins PJ;
 XX WPI; 2000-182542/16.
 XX A new therapeutic agent comprising a conjugate for treating secondary
 PT tissue damage and other disease conditions like Alzheimer's disease,
 PT stroke, Parkinson's disease and atherosclerosis.
 XX Disclosure; Page 60; 204pp; English.
 XX The present sequence represents a chemokine receptor ligand. The present
 CC ligand can be incorporated into the conjugates of the invention. The
 CC specification describes a conjugate, comprising a targeted agent and a
 CC chemokine receptor ligand. The conjugate binds to a chemokine receptor
 CC resulting in internalisation of the targeted agent in cells bearing the
 CC receptor. The conjugates are used for formulating a medicament or for
 CC treating disorders associated with inflammatory responses resulting from
 CC activation, proliferation and migration of immune effector cells. The
 CC disorders or disease states comprise secondary tissue damage such as
 CC central nervous system (CNS) injury, CNS inflammatory diseases,
 CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
 CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
 CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
 CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
 CC regulated cancers

QY 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

Query Match 100.0%; Score 405; DB 3; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCCYFNFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 4
 AAO20010
 ID AAO20010 standard; protein; 76 AA.
 XX
 XX AAO20010;
 XX 11-JUN-2002 (first entry)
 DT Human chemokine MCP-1 protein.
 DE Human; chemokine; anti-HIV; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; dermatological; anti-inflammatory; anti-allergic;
 KW

KW immunosuppressive; polymer-modified bioactive synthetic chemokine; HIV;
 KW AIDS; asthma; allergic rhinitis; atopic dermatitis; rheumatoid arthritis;
 KW atheroma; atherosclerosis; organ transplant rejection; MCP-1.
 XX Homo sapiens.
 OS
 XX WO200204015-A1.
 PN
 XX
 XX
 PD 17-JAN-2002.
 XX
 PF 12-JUL-2001; 2001WO-US021933.
 XX
 XX 12-JUL-2000; 2000US-0217683P.
 PR
 XX (GRYP-) GRYPHON SCI.
 PA
 XX Kochoendoerfer G, Botti P, Bradburne JA, Chen S, Cressman S;
 PI
 XX WPI; 2002-268857/31.
 DR
 XX
 XX New polymer-modified bioactive synthetic chemokines useful in the
 PT treatment of various diseases or disorders e.g. asthma.
 XX
 XX Claim 8; Fig 10A; 176pp; English.
 PS
 XX The invention relates to polymer-modified bioactive synthetic chemokines
 CC and to methods for their production and use. The compounds and methods of
 CC the backbone of the invention are useful in the analysis and treatment of
 CC various diseases states e.g. HIV and AIDS related disorders, asthma,
 CC allergic rhinitis, atopic dermatitis, atheroma/atherosclerosis, organ
 CC transplant rejection, and rheumatoid arthritis. This sequence represents
 CC the human chemokine MCP-1 protein of the invention
 XX
 SQ Sequence 76 AA;
 Query Match 100.0%; Score 405; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76
 RESULT 5
 ID AAO14143 standard; protein; 76 AA.
 AC AAO14143;
 XX
 XX 25-APR-2002 (first entry)
 DT Human MCP-1 protein.
 DE
 XX Human; chemokine receptor modulator; chemokine; HIV infection; AIDS;
 KW asthma; allergic rhinitis; atopic dermatitis; atheroma; antiinflammatory;
 KW antiasthmatic; antiallergic; dermatological; antiarteriosclerotic;
 KW antirheumatic; antiarthritic; anti-HIV; immunosuppressive; MCP-1;
 KW atherosclerosis; organ transplant rejection; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 XX WO200204499-A1.
 PN
 XX
 PD 17-JAN-2002.
 XX
 PF 12-JUL-2001; 2001WO-US021934.
 XX
 XX 12-JUL-2000; 2000US-0217683P.
 PR

(GRYP-) GRYPHON SCI.
 Offord R, Gaertner H, Hartley O;
 WPI; 2002-171703/22.
 Chemokine receptor modulator useful for treating e.g. asthma, allergic
 rhinitis comprises a chemically modified carboxyl-terminus and/or amino
 terminus analogs.
 Example 3; Fig 2; 86pp; English.
 The present invention relates to chemokine receptor modulators, which
 comprise a chemokine polypeptide chain modified at N-terminus with an
 aliphatic chain and at least one amino acid derivatives and/or modified
 at its C-terminus with an aliphatic chain or polycyclic. The modulators
 can be used to treat diseases such as HIV infection, AIDS, asthma, allergic
 rhinitis, atopic dermatitis, atheroma, atherosclerosis, organ
 transplant rejection and rheumatoid arthritis. The present sequence is
 the human MCP-1 protein
 Sequence 76 AA;
 Query Match 100.0%; Score 405; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76
 RESULT 6
 ID AAM53048 standard; protein; 76 AA.
 AC AAM53048;
 XX
 XX 26-MAR-2002 (first entry)
 DT Human monocyte chemoattractant protein-1 (MCP-1).
 DE
 XX Human; monocyte chemoattractant protein-1; MCP-1; C-C chemokine family;
 KW pulmonary hypertension; primary; hypotensive.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 2..8
 FT /note= "These residues are deleted in a specifically
 FT claimed human MCP-1 mutant, 7ND-MCP-1 (AAM53049)"
 XX
 XX WO200189582-A1.
 XX
 XX 29-NOV-2001.
 XX
 XX 25-MAY-2001; 2001WO-JP004381.
 XX
 XX 26-MAY-2000; 2000JP-00161145.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX (EGAS/) EGASHIRA K.
 XX
 XX Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y;
 WPI; 2002-083059/11.
 DR N-PSDB; ABA02497.
 XX

PT Preventives and remedies for pulmonary hypertension containing mutant of
PT MCP-1 antagonistic inhibitory type or its salt, encoded DNA or
PT neutralization antibody.
XX
PS Disclosure; Page 31; 39pp; Japanese.
XX
CC The invention relates to preventives and remedies for pulmonary
CC hypertension, comprising an antagonistic inhibitory mutant of monocyte
CC chemoattractant protein-1 (MCP-1), DNA encoding the mutant MCP-1, or a
CC neutralising antibody against MCP-1. MCP-1 is a member of the C-C
CC chemokine family. The preventives and remedies have hypotensive activity
CC and can be used in the prevention and treatment of pulmonary hypertension
CC particularly pulmonary primary hypertension. The present sequence
XX represents wild-type human MCP-1
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 8.7e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCVNFTRNKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
DB 1 QPDAINAPVTCVNFTRNKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
QY 61 QDSMDHLKQQTPTKT 76
DB 61 QDSMDHLKQQTPTKT 76
RESULT 7
ADC89673
ID ADC89673 standard; protein; 76 AA.
AC ADC89673;
XX
XX
DT 01-JAN-2004 (first entry)
XX
DE Human mature MCP-1 SEQ ID NO:4.
XX
XX human; MCP-1; monocyte chemoattractant protein; MCP; immunosuppressive;
KW antiinflammatory; cytosolic; antimicrobial; vasotropic; gene therapy;
KW MCP-2; MCP-3; MCP-4; Boraxin; leukocyte migration; leukocyte activation;
KW vascular disorder; cancer; inflammation; autoimmune disease; infection.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003084993-A1.
XX
XX 16-OCT-2003.
XX
XX 09-APR-2003; 2003WO-EP050097.
XX
XX 10-APR-2002; 2002US-0371442P.
XX
XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
XX Proudfoot A, Kosco-Vilbois M, Handel T;
XX WPI; 2003-804294/75.
XX
XX New antagonists of MCP proteins, useful in preparing a composition for
XX treating or preventing diseases related to excessive leukocyte migration
XX and activation e.g. vascular, inflammatory or autoimmune disease, cancer
XX or infection.
XX
XX Example 3; SEQ ID NO 4; 63pp; English.
XX
XX The invention relates to novel antagonists of MCP proteins comprising
XX mutants of MCP proteins in which the following combinations of residues,
XX numbered on the sequence of human mature MCP-1, are substituted to
XX Alanine, Glycine, Serine, Threonine, Proline, Aspartic Acid, Asparagine,

CC Glutamic Acid or Glutamine; 18 and 19; 18 and/or 19, together with 58; 18
CC and/or 19, together with 66; 18 and/or 19, together with 58 and 66; and
CC 18 and/or 19, together with 24, 44, 49 and/or 75. A protein of the
CC invention has immunosuppressive, antiinflammatory, cytostatic,
CC antimicrobial, and vasotropic activity. The protein may have a use in
CC gene therapy, and in a vaccine. The MCP proteins are human MCP-1, human
CC MCP-2, human MCP-3, human MCP-4 or human Eotaxin. The MCP antagonists are
CC useful in preparing a composition for treating or preventing diseases
CC related to excessive leukocyte migration and activation, e.g., vascular
CC disorders, cancer, inflammatory or autoimmune disease or infection. The
CC present sequence is used in the exemplification of the invention.
XX
XX Sequence 76 AA;
Query Match 100.0%; Score 405; DB 7; Length 76;
Best Local Similarity 100.0%; Pred. No. 8.7e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCVNFTRNKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
DB 1 QPDAINAPVTCVNFTRNKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
QY 61 QDSMDHLKQQTPTKT 76
DB 61 QDSMDHLKQQTPTKT 76
RESULT 8
ADD14998
ID ADD14998 standard; protein; 76 AA.
XX
XX ADD14998;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human monocyte chemoattractant protein-1 (MCP-1) mature protein.
XX
XX antiinflammatory; MCP-1 Antagonist; biocompatibility; medical device;
KW monocyte chemoattractant protein 1; MCP-1; MCP-1 antagonist;
KW chronic inflammation; fibrous encapsulation; human.
XX
XX Homo sapiens.
XX
XX US2003129214-A1.
XX
XX 10-JUL-2003.
XX
XX 09-JAN-2003; 2003US-0033977B.
XX
XX 10-JAN-2002; 2002US-0347560P.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Bornstein P, Kyriakides T;
XX WPI; 2003-787133/74.
XX N-PSDB; ADD14996.
XX
XX Enhancing biocompatibility of a medical device implanted in a portion of
XX a living body by contacting the portion of the body that is in contact
XX with the implanted device with monocyte chemoattractant protein 1 (MCP-1)
XX antagonist.
XX
XX Disclosure; SEQ ID NO 3; 18pp; English.
XX
XX The invention describes a method of enhancing (M1) the biocompatibility
XX of a medical device implanted within a portion of a living body
XX comprising contacting a portion of the living body in contact with the
XX device with a monocyte chemoattractant protein 1 (MCP-1) antagonist to
XX inhibit chronic inflammation induced by the presence of the medical
XX device or fibrous encapsulation of the medical device. The method is
XX useful for enhancing the biocompatibility of a medical device implanted
XX in a portion of a living body by inhibiting chronic inflammation or

CC formation of fibrous capsules around the device. This is the amino acid
 CC sequence of human monocyte chemoattractant protein-1 (MCP-1) mature
 CC protein.
 XX
 SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNKRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNTNKRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 9

ADE80852
 ID ADE80852 standard; peptide; 76 AA.

AC ADE80852;

DT 29-JAN-2004 (first entry)

DE huMCP1 chemokine.

XX Nuclear targeting peptide; nuclear targeting domain; Eskine; PESKY;
 KW chemokine; cancer; cytostatic; huMCP1; chemokine.
 XX

OS Unidentified.

XX WO2003082920-A1.

XX 09-OCT-2003.

XX 02-APR-2003; 2003WO-GB001472.

XX 02-APR-2002; 2002GB-00007624.

XX (CANC-) CANCER RES TECHNOLOGY LTD.

XX Graham G;

XX WPI; 2003-788341/74.

XX New nuclear targeting peptide comprising a nuclear targeting domain
 PT isolated from a chemokine, useful for preparing a medicament for treating
 PT cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma.
 XX

PS Disclosure; Fig 11; 66pp; English.

XX The present invention relates to a nuclear targeting peptide (ADE80826)
 CC comprising a nuclear targeting domain isolated from the C-terminal
 CC sequence of the Eskine and PESKY chemokines. The nuclear targeting domain
 CC allows the protein to translocate to the cell nucleus. The nuclear
 CC targeting peptide is useful in preparing a medicament for treating
 CC cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma. The
 CC present sequence is a chemokine sequence, used in a sequence alignment in
 CC the invention.
 XX

SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNKRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNTNKRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 10

ADE06777
 ID ADE06777 standard; protein; 76 AA.

XX ADE06777;

XX 29-JAN-2004 (first entry)

XX Human MCP-1 SEQ ID NO:1.

XX human; MCP-1; monocyte chemoattractant protein-1; immunosuppressive;
 KW cardiant; neuroprotective; antimicrobial; cytostatic; gene therapy;
 KW immune disorder; cardiovascular disorder; neurological disorder;
 KW infectious disorder; malignant disorder.
 XX

XX Homo sapiens.

XX WO2003083059-A2.

XX 09-OCT-2003.

XX 24-MAR-2003; 2003WO-US009056.

XX 26-MAR-2002; 2002US-0367932P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Das A;

XX WPI; 2003-804039/75.

XX New monocyte chemoattractant protein-1 (MCP-1) mutein nucleic acid,
 PT useful for diagnosing or treating a MCP-1 mutein-related condition, e.g.
 PT immune, cardiovascular, neurologic or infectious or malignant disorders.
 XX

PS Claim 1; SEQ ID NO 1; 81pp; English.

XX The invention relates to a novel monocyte chemoattractant protein-1 (MCP-
 CC 1) mutant nucleic acid. A protein of the invention has immunosuppressive,
 CC cardiant, neuroprotective, antimicrobial, and cytostatic activity. A
 CC polynucleotide of the invention may have a use in gene therapy. The
 CC protein, nucleic acid, composition and method are useful for diagnosing
 CC or treating a MCP-1 mutein-related condition, e.g. immune,
 CC cardiovascular, neurologic or infectious or malignant disorders. The
 CC present sequence represents human MCP-1.

XX Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.7e-43;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNKRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
 DB 1 QPDAINAPVTCYNTNKRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76

DB 61 QDSMDHLDKQTQTPKT 76

RESULT 11

AAP95387
 ID AAP95387 standard; protein; 99 AA.

XX AAP95387;

XX 25-MAR-2003 (revised)

PF 28-SEP-1994; 94WO-CA000516.
XX
PR 28-SEP-1993; 93US-00127499.
XX
PA (VALS/) VAN ALSTYNE D.
PA (SHAR/) SHARMA L R.
XX
PI Van Alstyne D, Sharma LR;
XX
XX WPI; 1995-147431/19.
DR
XX New peptide(s) and corresp. antibodies for the treatment of meningitis -
PT the peptide(s) corresp. to homologous antigenic sites on bacterial and
PT viral agents and on chemokine(s), used for detecting and preventing
PT meningitis.
XX
XX Claim 47; Fig 8/10; 98pp; English.
PS
XX AAR73914 is the chemokine Human monocyte chemoattractant factor hMCP-1.
CC It contains the meningitis related antigenic sequences (MRHAS) claimed in
CC AAR73895 and AAR73907, which are recognised by a monoclonal antibody from
CC the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be
CC used in immunoassays to diagnose the presence of bacterial and/or viral
CC meningitis agents in a sample, or in prophylactic and therapeutic
CC meningitis treatments. The peptides may also be used as vaccines against
CC meningitis. NB: Identified by matching corresponding MRHAS peptides.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 99 AA;
SQ
Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99
RESULT 14
AAR70800
ID AAR70800 standard; protein; 99 AA.
XX
AC AAR70800;
XX
XX 25-MAR-2003 (revised)
DT 29-AUG-1995 (first entry)
XX
DE Chemoattractant protein MCP-1.
XX
XX MCP-1; chemoattractant; heparanase; heparin; heparan sulfate; arthritis;
KW restenosis; cancer; wound healing.
XX
XX Homo sapiens.
OS
XX W09504158-A1.
PN
XX
XX 09-FEB-1995.
PD
XX
XX 26-JUL-1994; 94WO-US008207.
PF
XX
XX 29-JUL-1993; 93US-00099866.
PR 13-OCT-1993; 93US-00136117.
XX
XX (UPJO) UPJOHN CO.
PA
XX
XX Hoogwerf AJ, Ledbetter SR;
PI
XX WPI; 1995-082239/11.
DR

DR N-PSDB; AAQ85370.
XX
PT Screening for cpds. with anti-heparanase activity - by detecting
PT inhibition of heparin or heparan sulphate degradation, potentially useful
PT for treating arthritis, restenosis, cancer.
XX
XX Claim 13; Page 49; 60pp; English.
PS
XX Purified heparanases, prepared under reducing conditions and activated
CC with transglutaminase, are given in AAR70786-804. Most are prepared by
CC reverse transcription of mRNA from activated human leukocytes, then
CC cloning of the cDNA into pVL1392 baculovirus vector, and expression in
CC Sf9 cells in the presence of reduced glutathione and dithiothreitol.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 99 AA;
SQ
Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99
RESULT 15
AAR70174
ID AAR70174 standard; protein; 99 AA.
XX
AC AAR70174;
XX
XX 01-JUL-1998 (first entry)
DT
XX
DE Macrophage chemoattractant peptide designated MCP-1.
XX
XX Monocyte chemoattractant peptide; MCP; MCP-1; treatment; neoplasm;
KW infection; human; monocyte receptor; chemotactic response; inflammation;
KW monocyte infiltration.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 37..39
FT /note= "potential N-linked glycosylation site"
XX
XX US5714578-A.
PN
XX
XX 03-FEB-1998.
PD
XX
XX 06-JUN-1995; 95US-00466280.
PF
XX
XX 31-JAN-1989; 89US-00304234.
PR 30-MAR-1989; 89US-00330446.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Leonard EJ, Appella E, Robinson EA, Yoshimura T;
PI
XX WPI; 1998-129909/12.
DR N-PSDB; AAV10341.
XX
XX Peptide with chemotactic activity for monocytes - from human monocytes or
PT glioma cells, useful for treating infections and neoplasms.
XX
XX Disclosure; Fig 2; 21pp; English.
PS
XX The present sequence represents a monocyte chemoattractant peptide (MCP)
CC designated MCP-1. MCPs can be isolated from human glioma cell line U-

CC 105MG and peripheral blood mononuclear leukocytes. MCPs are used for the
CC treatment of neoplasms and infections in humans. Short peptides derived
CC from MCPs can be screened to identify those that can bind to the monocyte
CC receptor without stimulating a chemotactic response. These are
CC potentially useful for treating inflammation associated with monocyte
CC infiltration
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 405; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDALNAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKW 60
Db 24 QPDALNAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKW 83
QY 61 QDSMDHLDKQTTPKT 76
Db 84 QDSMDHLDKQTTPKT 99

Search completed: August 30, 2004, 17:04:49
Job time : 126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 17:07:28 ; Search time 129 Seconds
(without alignments)
195.353 Million cell updates/sec

Title: 07330446.PEP
Perfect score: 405
Sequence: 1 qpdaainapvtccynftnrki.....qkwvqdamdhldkgtqtpkt 76
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1297172 seqs, 314612898 residues
Total number of hits satisfying chosen parameters: 1297172
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pap.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pap.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pap.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	76	9	US-09-195-457-5
2	405	100.0	76	9	US-09-792-793A-20
3	405	100.0	76	14	US-10-339-778-3
4	405	100.0	76	14	US-10-276-971-1
5	405	100.0	76	15	US-10-375-209A-20
6	405	100.0	76	16	US-10-332-038A-5
7	405	100.0	76	16	US-10-668-733-7
8	405	100.0	76	16	US-10-668-733-14
9	405	100.0	78	16	US-10-803-960-14
10	405	100.0	98	12	US-10-449-831A-210
11	405	100.0	99	8	US-09-927-939-16
12	405	100.0	99	10	US-09-920-137A-9
13	405	100.0	99	12	US-10-054-967-5
14	405	100.0	99	12	US-10-170-385-395
15	405	100.0	99	13	US-10-057-275-9

16	405	100.0	99	13	US-10-033-067-4	Sequence 4, Appli
17	405	100.0	99	13	US-10-141-965-5	Sequence 5, Appli
18	405	100.0	99	14	US-10-146-496-9	Sequence 9, Appli
19	405	100.0	99	14	US-10-293-705-8	Sequence 8, Appli
20	405	100.0	99	14	US-10-137-655-9	Sequence 9, Appli
21	405	100.0	99	15	US-10-116-275-222	Sequence 22, App
22	405	100.0	99	15	US-10-440-464-62	Sequence 62, Appli
23	405	100.0	99	16	US-10-764-649-18	Sequence 18, Appli
24	405	100.0	122	14	US-10-339-778-2	Sequence 2, Appli
25	405	100.0	133	12	US-10-449-831A-214	Sequence 214, App
26	405	100.0	325	9	US-09-792-793A-71	Sequence 71, Appli
27	405	100.0	325	15	US-10-375-209A-71	Sequence 71, Appli
28	405	100.0	327	9	US-09-792-793A-72	Sequence 72, Appli
29	405	100.0	327	15	US-10-375-209A-72	Sequence 72, Appli
30	405	100.0	332	9	US-09-792-793A-73	Sequence 73, Appli
31	405	100.0	332	15	US-10-375-209A-73	Sequence 73, Appli
32	398	98.3	99	9	US-09-834-795A-28	Sequence 28, Appli
33	398	98.3	99	10	US-09-834-794A-28	Sequence 28, Appli
34	362	89.4	69	14	US-10-339-778-4	Sequence 4, Appli
35	362	89.4	69	14	US-10-276-971-2	Sequence 2, Appli
36	357	88.1	90	12	US-10-424-599-263303	Sequence 263303,
37	293	72.3	97	10	US-09-920-137A-5	Sequence 5, Appli
38	293	72.3	97	13	US-10-057-275-5	Sequence 5, Appli
39	293	72.3	97	14	US-10-137-655-5	Sequence 5, Appli
40	287	70.9	76	9	US-09-792-793A-22	Sequence 22, Appli
41	287	70.9	76	12	US-10-646-770-19	Sequence 19, Appli
42	287	70.9	76	14	US-10-125-451-19	Sequence 19, Appli
43	287	70.9	76	14	US-10-263-139-19	Sequence 19, Appli
44	287	70.9	76	15	US-10-375-209A-22	Sequence 22, Appli
45	287	70.9	76	16	US-10-332-038A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. US20020081623A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9319884.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-09-195-457-5

Query Match	100.0%	Score 405;	DB 9;	Length 76;
Best Local Similarity	100.0%	Pred. No. 4.6e-43;		
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			0;	Indels
				Gaps
				0;
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Db	1	QPDAINAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTTIVAKEICADPKQKWV	60	
Qy	61	QDSWDHLDKOTQTPKT	76	

Db 61 QDSMDHLKQTQTPKT 76

RESULT 2
US-09-792-793A-20
; Sequence 20, Application US/09792793A
; Patent No. US20020169370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-09-792-793A-20

Query Match 100.0%; Score 405; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 3
US-10-339-778-3
; Sequence 3, Application US/10339778
; Publication No. US20030129214A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, P.
; APPLICANT: Kyriakides, T.
; TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC
; TITLE OF INVENTION: DEVICE
; FILE REFERENCE: UNOTL-1-20275
; CURRENT APPLICATION NUMBER: US/10/339,778
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,560
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 3
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-339-778-3

Query Match 100.0%; Score 405; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 4
US-10-276-971-1
; Sequence 1, Application US/10276971
; Publication No. US20030162737A1
; GENERAL INFORMATION:
; APPLICANT: Egashira Kensuke
; APPLICANT: Yoshikazu Yonemitsu
; APPLICANT: Katsuo Sueishi
; APPLICANT: Yasuhiro Ikeda
; APPLICANT: Yoshiyuki Inada
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
; FILE REFERENCE: 2733 USOP
; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Human
US-10-276-971-1

Query Match 100.0%; Score 405; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 5
US-10-375-209A-20
; Sequence 20, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-10-375-209A-20

Query Match 100.0%; Score 405; DB 15; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 6
US-10-332-038A-5
; Sequence 5, Application US/10332038A
; Publication No. US20040077835A1

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; GENERAL INFORMATION:
; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Offord, Robin
; APPLICANT: Gaertner, Hubert
; APPLICANT: Hattley, Oliver
; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
; FILE REFERENCE: 03504.271
; CURRENT APPLICATION NUMBER: US/10/332.038A
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US 60/217,683
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-5

Query Match      100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 7
US-10-668-733-7
; Sequence 7, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-7

Query Match      100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 8
US-10-668-733-14
; Sequence 8, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-14

Query Match      100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 9
US-10-803-960-14
; Sequence 9, Application US/10803960
; Publication No. US20040156822A1
; GENERAL INFORMATION:
; APPLICANT: White, John R.
; APPLICANT: Pelus, Louis
; APPLICANT: Li, Haodong
; APPLICANT: Kreider, Brent L.
; TITLE OF INVENTION: Novel Chemokine for Mobilizing Stem Cells
; FILE REFERENCE: PF497D2
; CURRENT APPLICATION NUMBER: US/10/803,960
; PRIOR FILING DATE: 2004-03-19
; CURRENT APPLICATION NUMBER: 09/567,225
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/225,501
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/006,051
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: US 08/740,033
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 78
; TYPE: PRT
; ORGANISM: MCP-1
US-10-803-960-14

Query Match      100.0%; Score 405; DB 16; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 3 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

QY 61 QDSMDHLDKQTQTPKT 76
Db 63 QDSMDHLDKQTQTPKT 78
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; Sequence 14, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-14

Query Match      100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 9
US-10-803-960-14
; Sequence 14, Application US/10803960
; Publication No. US20040156822A1
; GENERAL INFORMATION:
; APPLICANT: White, John R.
; APPLICANT: Pelus, Louis
; APPLICANT: Li, Haodong
; APPLICANT: Kreider, Brent L.
; TITLE OF INVENTION: Novel Chemokine for Mobilizing Stem Cells
; FILE REFERENCE: PF497D2
; CURRENT APPLICATION NUMBER: US/10/803,960
; PRIOR FILING DATE: 2004-03-19
; CURRENT APPLICATION NUMBER: 09/567,225
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/225,501
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/006,051
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: US 08/740,033
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 78
; TYPE: PRT
; ORGANISM: MCP-1
US-10-803-960-14

Query Match      100.0%; Score 405; DB 16; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 3 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

QY 61 QDSMDHLDKQTQTPKT 76
Db 63 QDSMDHLDKQTQTPKT 78
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RESULT 10
US-10-449-831A-210
; Sequence 210, Application US/10449831A
; Publication No. US20040029179A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; TITLE OF INVENTION: Higher molecular weight entities and uses therefor
; FILE REFERENCE: 2385978
; CURRENT FILING DATE: 2003-05-30
; CURRENT APPLICATION NUMBER: US/10/449,831A
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: USSN 60/384878
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human
US-10-449-831A-210

Query Match 100.0%; Score 405; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 6.2e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDANAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKQKW 60
DB 23 QPDANAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKQKW 82
QY 61 QDSMDHLDKQTQTPKT 76
DB 83 QDSMDHLDKQTQTPKT 98

RESULT 11
US-08-927-939-16
; Sequence 16, Application US/08927939
; Publication No. US2001000640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295,022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-16

Query Match 100.0%; Score 405; DB 8; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDANAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKQKW 60
DB 24 QPDANAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 12
US-09-920-137A-9
; Sequence 9, Application US/09920137A
; Publication No. US20030049725A1
; GENERAL INFORMATION:
```

```
APPLICANT: Coleman, Roger
APPLICANT: Bandman, Olga
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/920,137A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: MCP-1
US-09-920-137A-9

Query Match 100.0%; Score 405; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDANAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKQKW 60
DB 24 QPDANAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 13
US-10-054-967-5
; Sequence 5, Application US/10054967
; Publication No. US2003005987A1
; GENERAL INFORMATION:
; APPLICANT: KREIDER, BRENT L.
; RUBEN, STEVEN M.
; OLSEN, HENRIK S.
TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,967
FILING DATE: 25-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/995,156
FILING DATE: 19-DEC-1997
APPLICATION NUMBER: 60/042,269
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-054-967-5

Query Match 100.0%; Score 405; DB 12; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 14

US-10-170-385-395
Sequence 395, Application US/10170385
Publication No. US20030203372A1
GENERAL INFORMATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Mundy, Christopher Robert
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 395
LENGTH: 99
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-170-385-395

Query Match 100.0%; Score 405; DB 12; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 15

US-10-057-275-9
Sequence 9, Application US/10057275
Publication No. US2002015545A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
Bandman, Olga
Wildie, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/057,275
FILING DATE: 25-Jan-2002
PRIOR APPLICATION NUMBER: US/08/390,740A
FILING DATE: February 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: MCP-1
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-057-275-9

Query Match 100.0%; Score 405; DB 13; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

Search completed: August 30, 2004, 17:19:01
Job time : 131 secs

Wed Sep 1 08:47:04 2004

07330446.pap.rapb

Page 6

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OM protein - protein search, using sw model

Run on: August 30, 2004, 16:52:21 ; Search time 24 Seconds
(without alignments)
164.889 Million cell updates/sec

Title: 07330446.PEP
Perfect score: 405
Sequence: 1 qpdainapvccynftnrki.....qkwvqdsmdhldkgtqtpkt 76

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	99	1 SY02 HUMAN	P13500 homo sapien
2	394	97.3	99	1 SY02 WACPA	Q8MYN4 macaca fasc
3	337	83.2	99	1 SY02 PIG	P42831 sus scrofa
4	331	81.7	101	1 SY02 CANFA	P52203 canis fami
5	315	77.8	99	1 MCPA BOVIN	P28291 bos taurus
6	314	77.5	125	1 SY02 RABIT	P28292 oryctolagus
7	308	76.0	74	1 MCPB BOVIN	P80343 bos taurus
8	287	70.9	99	1 SY07 HUMAN	P80098 homo sapien
9	284	70.1	104	1 SY12 MOUSE	Q24401 mus musculu
10	273	67.4	97	1 EOTA HUMAN	P51671 homo sapien
11	268	66.2	99	1 SY08 HUMAN	P80075 homo sapien
12	261	64.4	99	1 SY08 PIG	P49873 sus scrofa
13	253.5	62.6	98	1 SY13 HUMAN	Q99616 homo sapien
14	252	62.2	148	1 SY02 MOUSE	P10148 mus musculu
15	247	61.0	99	1 SY08 BOVIN	Q99141 bos taurus
16	241	59.5	148	1 SY02 RAT	P48444 rattus norv
17	236	59.3	120	1 SY02 CAVPO	Q08782 cavia porce
18	221	54.6	97	1 EOTA RAT	P97545 rattus norv
19	218	53.8	97	1 EOTA MOUSE	P48298 mus musculu
20	214	52.8	96	1 EOTA CAVPO	P80325 cavia porce
21	205	50.6	97	1 SY07 MOUSE	Q03366 mus musculu
22	202	49.9	97	1 SY07 RAT	Q9qxy8 rattus norv
23	177	43.7	97	1 SY08 MOUSE	Q92121 mus musculu
24	152	37.5	119	1 SY24 MOUSE	Q9jkc0 mus musculu
25	148.5	36.7	70	1 REG1 BOVIN	P82943 bos taurus
26	145.5	35.9	93	1 SY3L HUMAN	P16619 homo sapien
27	142.5	35.2	92	1 SY03 HUMAN	P10147 homo sapien
28	137	33.8	119	1 SY24 HUMAN	O00175 homo sapien
29	135.5	33.5	90	1 SY04 CHICK	Q90826 gallus gall
30	135.5	33.5	92	1 SY04 HUMAN	P3236 h small ind
31	133.5	33.0	92	1 SY04 RABIT	P46632 oryctolagus
32	133.5	33.0	92	1 SY04 RAT	P50230 rattus norv
33	131	32.3	393	1 SYD1 RAT	O55145 rattus norv

ALIGNMENTS

RESULT 1

SY02_HUMAN	SY02_HUMAN	STANDARD;	PRT;	99 AA.
AC	P13500; Q9UDF3;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein-1) (MCP-1) (Monocyte chemoattractant protein-1) (Monocyte chemoattractant and activating factor) (MCAF) (Monocyte secretory protein JE) (HC11).			
DE	CCL2 OR SCYA2 OR MCP1.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8915862; PubMed=2923622;			
RA	Furutani Y., Nomura H., Notake M., Oyama Y., Fukui T., Yamada M., Larsen C.G., Oppenheim J.J., Matsushima K.;			
RA	"Cloning and sequencing of the cDNA for human monocyte chemoattractant protein-1 (MCP-1) (Monocyte chemoattractant and activating factor) (MCAF).";			
RT	Biochem. Biophys. Res. Commun. 159:249-255(1989).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=90097880; PubMed=2513477;			
RX	Rollins B.J., Stier P., Ernst T., Wong G.G.;			
RA	"The human homolog of the JE gene encodes a monocyte secretory protein.";			
RT	Mol. Cell. Biol. 9:4687-4695(1989).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=89153605; PubMed=2465924;			
RX	Yoshimura T., Yuhki N., Moore S.K., Appella E., Lerman M.I., Leonard E.J.;			
RA	"Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JE.";			
RT	FEBS Lett. 244:487-493(1989).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=90290456; PubMed=2357211;			
RX	Shyu Y.J., Li Y.S., Kolattukudy P.E.;			
RA	"Structure of human monocyte chemoattractant protein gene and its regulation by TPA.";			
RT	Biochem. Biophys. Res. Commun. 169:346-351(1990).			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=91207938; PubMed=2518726;			
RX	Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;			
RA	"Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family.";			
RT	Int. Immunol. 1:388-399(1989).			
RL	[6]			
RN	SEQUENCE FROM N.A.			
RP				

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RX MEDLINE=94150478; PubMed=8107690;
RA Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F.,
RA Kolattukudy P.E.;
RT "The expression of monocyte chemoattractant protein (MCP-1) in human
RT vascular endothelium in vitro and in vivo";
RL Mol. Cell. Biochem. 126:61-68(1993).
RN [7]
RX SEQUENCE FROM N.A.
RX MEDLINE=92095166; PubMed=1661560;
RA Yoshimura T., Leonard E.J.;
RT "Human monocyte chemoattractant protein-1 (MCP-1).";
RL Adv. Exp. Med. Biol. 305:47-56(1991).
RN [8]
RX SEQUENCE FROM N.A.
RX MEDLINE=91301709; PubMed=2071154;
RA Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.;
RT "Assignment of the human small inducible cytokine A2 gene, SCYA2
RT (encoding JS or MCP-1), to 17q11.2-12: evolutionary relatedness of
RT cytokines clustered at the same locus";
RL Genomics 10:489-492(1991).
RN [9]
RX SEQUENCE FROM N.A.
RX MEDLINE=20374005; PubMed=10918580;
RA Finzer P., Soto U., Dellus H., Patzelt A., Pouetka A., Coy J.F.,
RA zur Hausen H., Roessl F.;
RT "Differential transcriptional regulation of the
RT monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and
RT non-tumorigenic HPV 18 positive cells: The role of the chromatin
RT structure and AP-1 composition";
RL Oncogene 19:3235-3244(2000).
RN [10]
RX SEQUENCE FROM N.A.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RX SEQUENCE FROM N.A.
RX TISSUE=Pancres;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RX SEQUENCE OF 24-99.
RX MEDLINE=89184525; PubMed=2648385;
RA Robinson E.A., Yoshimura T., Leonard E.J., Tanaka S., Griffin P.R.,
RA Shabanowitz J., Hunt D.F., Appella E.;
RT "Complete amino acid sequence of a human monocyte chemoattractant, a
RT putative mediator of cellular immune reactions";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854(1989).
RN [13]
RX SEQUENCE OF 29-53 AND 82-92.
RX MEDLINE=90211336; PubMed=2322286;
RA Decock B., Conings R., Lenaerts J.-P., Billiau A., van Damme J.;
RT "Identification of the monocyte chemoattractant protein from human
RT osteosarcoma cells and monocytes: detection of a novel N-terminally
processed form.";
Biochem. Biophys. Res. Commun. 167:904-909(1990).
RN [14]
RX 3D-STRUCTURE MODELING.
RX MEDLINE=91312872; PubMed=1857712;
RA Gronenborn A.M., Clore G.M.;
RT "Modeling the three-dimensional structure of the monocyte chemo-
RT attractant and activating protein MCP-1 on the basis of the
RT solution structure of interleukin-8";
RL Protein Eng. 4:263-269(1991).
RN [15]
RX X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=97143315; PubMed=8989326;
RA Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
RT "The structure of MCP-1 in two crystal forms provides a rare example
RT of variable quaternary interactions";
RL Nat. Struct. Biol. 4:64-69(1997).
RN [16]
RX STRUCTURE BY NMR.
RX MEDLINE=96234959; PubMed=8639605;
RA Handel T.M., Domaille P.J.;
RT "Heteronuclear (1H, 13C, 15N) NMR assignments and solution structure
RT of the monocyte chemoattractant protein-1 (MCP-1) dimer";
RL Biochemistry 35:6569-6584(1996).
RN [17]
RX EFFECT OF DELETION OF N-TERMINAL RESIDUES.
RX MEDLINE=96195223; PubMed=8627182;
RA Weber M., Ugucioni M., Baggioni M., Clark-Lewis I., Dahinden C.A.;
RT "Deletion of the NH2-terminal residue converts monocyte chemoattractant
RT protein 1 from an activator of basophil mediator release to an
RT eosinophil chemoattractant";
RL J. Exp. Med. 183:681-685(1996).
RN [18]
RX MUTAGENESIS.
RX MEDLINE=94253189; PubMed=8195247;
RA Zhang Y.J., Rutledge B.J., Rollins B.J.;
RT "Structure/activity analysis of human monocyte chemoattractant
RT protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein
RT that inhibits MCP-1-mediated monocyte chemotaxis";
RL J. Biol. Chem. 269:15918-15924(1994).
RN [19]
RX SUBUNIT.
RX MEDLINE=97053697; PubMed=8898111;
RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3";
RL FEBS Lett. 395:277-282(1996).
CC -/- FUNCTION: Chemoattractant factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Augments monocyte anti-tumor
CC activity. Has been implicated in the pathogenesis of diseases
CC characterized by monocyte infiltrates, like psoriasis, rheumatoid
CC arthritis or atherosclerosis. May be involved in the recruitment
CC of monocytes into the arterial wall during the disease process of
CC atherosclerosis. Binds to CCR2 and CCR4.
CC -/- SUBUNIT: Monomer or homodimer; in equilibrium.
CC -/- SUBCELLULAR LOCATION: Secreted.
CC -/- PTM: PROCESSING AT THE N-TERMINUS CAN REGULATE RECEPTOR AND TARGET
CC CELL SELECTIVITY. DELETION OF THE N-TERMINAL RESIDUE CONVERTS
CC IT FROM AN ACTIVATOR OF BASOPHIL TO AN EOSINOPHIL CHEMOATTRACTANT.
CC -/- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; M31626; AAA36330.1; -
DR EMBL; M30816; AAA36330.1; JOINED.
DR EMBL; M31625; AAA36330.1; JOINED.
DR EMBL; M24545; AAA18164.1; -

```
Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 60
    |||||
DB 24 QPDAINAPVTCYNTFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 83
    |||||

QY 61 QDSMDHLDKQTQTPK 76
    |||||
DB 84 QDSMDHLDKQTQTPK 99
    |||||

RESULT 2
SY02_MACFA
ID SY02_MACFA STANDARD; PRT; 99 AA.
AC Q9WNI4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein-1) (MCP-1) (Monocyte chemoattractant protein-1).
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN CCL2 OR SCYA2 OR MCP1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis;
RA Studer C., Ufer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant protein-1."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mullatta;
RA Studer C., Ufer R.;
RT "Cloning and expression of rhesus monkey monocyte chemoattractant protein-1."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes and basophils but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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CC
CC EMBL; AF276081; AAF61899.1; -
CC EMBL; AF255343; AAF67756.1; -
CC HSSP; P13500; 1DOK.
CC InterPro; IPR000827; CC chemokine sm1.
CC InterPro; IPR001811; Chemokine_IL8.
CC InterPro; IPR008097; Fractalkine.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR01721; FRACTALKINE.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CC Cytokine; Chemotaxis; Signal; Inflammatory response;
KW Pyroldione carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
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FT MOD_RES 24 24 PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 99 AA; 11007 MW; 433CB8C64EE7A4F CRC64;

Query Match 97.3%; Score 394; DB 1; Length 99;
Best Local Similarity 98.7%; Pred. No. 3e-39;
Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 60
    |||||
DB 24 QPDAINAPVTCYNTFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKETICADPKQKW 83
    |||||

QY 61 QDSMDHLDKQTQTPK 75
    |||||
DB 84 QDSMDHLDKQTQTPK 98
    |||||

RESULT 3
SY02_PIG
ID SY02_PIG STANDARD; PRT; 99 AA.
AC P42831;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein-1) (MCP-1) (MCP-1) (Monocyte chemoattractant protein-1).
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN CCL2 OR SCYA2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94183284; PubMed=7510952;
RX Hosang X., Knoke I., Klaudiny J., Wempe F., Wuttke W., Scheit K.H.;
RA "Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): analysis by polymerase chain reaction and cDNA cloning.";
RL Biochem. Biophys. Res. Commun. 199;962-968(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Zach O.R.F.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes, but not neutrophils.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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CC
CC EMBL; Z48479; CAA88370.1; -
CC EMBL; X79416; CAA55945.1; -
CC FIR; JC2136; JC2136.
CC HSSP; P13500; 1DOK.
CC InterPro; IPR000827; CC chemokine sm1.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CC Cytokine; Chemotaxis; Signal; Inflammatory response;
KW Pyroldione carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
```

FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 101 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 99 AA, 10976 MW, 4COAC6278D4FOA09 CRC64;
Query Match 83.2%; Score 337; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.4e-32; Indels 0; Gaps 0;
Matches 60; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCYCNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIYAKETICADPKQKWV 60
DB 24 QPDALISPVTCYTLTKKISQRLASRYRITSSKCPKEAVIFKTIYAKETICADPKQKWV 83
QY 61 QDSMDHLDK--QTQPK 75
DB 84 QDSISHLDKKQTPK 98
RESULT 4
SY02_CANFA STANDARD; PRT; 101 AA.
ID SY02_CANFA
AC P52203;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN CCL2 OR SCYA2 OR MCP1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_SEQUENCE FROM N.A.
RC TISSUE=Jugular vein endothelial;
RC MEDLINE=97176620; PubMed=9024159;
RA Kumar A.G., Ballantyne C.M., Michael L.H., Kukiela G.L., Youker K.A.,
RA Lindsey M.L., Hawkins H.K., Birdsall H.H., Mackay C.R., Larosa G.J.,
RA Rossen R.D., Smith C.W., Entman M.L.;
RT "Induction of monocyte chemoattractant protein-1 in the small veins
RT of the ischemic and reperfused canine myocardium."
RL Circulation 95:693-700(1997).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils. Important factor in the course of the inflammatory
CC reaction to reperfusion of the previously ischemic myocardium.
CC May play a significant role in monocyte trafficking into the
CC reperfused myocardium.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Endothelium of small veins and intrafascicular
CC veins, and infiltrating leukocytes.
CC -!- INDUCTION: By TNF-alpha.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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CC EMBL; U29653; AAA84911.1; -
DR HSP; P13500; IDOM.
DR InterPro; IPR000827; CC Chemokine sm1.
DR InterPro; IPR001811; Chemokine IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRCTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR Cytokine; Chemotaxis; Signal; Inflammatory response;
KW Pyrolidone carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 101 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 101 AA, 11121 MW, CDD7E2B1901A7267 CRC64;
Query Match 81.7%; Score 331; DB 1; Length 101;
Best Local Similarity 80.5%; Pred. No. 7e-32; Indels 2; Gaps 1;
Matches 62; Conservative 7; Mismatches 5; Indels 2; Gaps 1;
QY 1 QPDAINAPVTCYCNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIYAKETICADPKQKWV 60
DB 24 QPDALISPVTCYTLTKKISQRLASRYRITSSKCPKEAVIFKTIYAKETICADPKQKWV 83
QY 61 QDSMDHLDK--QTQPK 75
DB 84 QDSMAHLDKKQTPAK 100
RESULT 5
MCPA_BOVIN STANDARD; PRT; 99 AA.
ID MCPA_BOVIN
AC P28291;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic
DE seminal fluid protein).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE FROM N.A.
RC TISSUE=Seminal plasma;
RC MEDLINE=92096117; PubMed=1721821;
RA Wempe F., Henschen A., Scheit K.H.;
RT "Gene expression and cDNA cloning identified a major basic protein
RT constituent of bovine seminal plasma as bovine
RT monocyte-chemoattractant protein-1 (MCP-1).";
RL DNA Cell Biol. 10:671-679(1991).
RN [2]
RC TISSUE=Seminal plasma;
RC TISSUE=Seminal plasma;
RC MEDLINE=92181448; PubMed=1543494;
RA Wempe F., Einspanier R., Scheit K.H.;
RT "Characterization by cDNA cloning of the mRNA of a new growth factor
RT from bovine seminal plasma: acidic seminal fluid protein.";
RL Biochem. Biophys. Res. Commun. 193:232-237(1992).
RN [3]
RC TISSUE=Seminal plasma;
RC TISSUE=Seminal plasma;
RC MEDLINE=94338337; PubMed=8060303;
RA Wempe F., Kuhlmann J.K., Scheit K.H.;
RT "Characterization of the bovine monocyte chemoattractant protein-1
RT gene.";
RL Biochem. Biophys. Res. Commun. 202:1272-1279(1994).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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CC or send an email to license@isb-sib.ch).
CC EMBL; L32659; AAA60956.1; -
DR

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DR EMBL; M84602; AAA30651.1; -.
DR PIR; A39296; A39296.
DR HSP; P13500; 1DOM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR CYTOKINE; Chemotaxis; Signal; Inflammatory response; Glycoprotein;
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 125 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 34 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;
Query Match 77.5%; Score 314; DB 1; Length 125;
Best Local Similarity 75.0%; Pred. No. 8.6e-30;
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCVYFNTRKISVQRLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDVNSPVTCVYFNTRKISVQRLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLKQQTPTK 76
Db 84 QDAIANLKKMQTPTK 99
RESULT 7
MCPB_BOVIN STANDARD; PRT; 74 AA.
ID MCPB_BOVIN STANDARD; PRT; 74 AA.
AC P80343;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Monocyte chemotactic protein 1B (MCP-1B) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RC TISSUE=Kidney;
RX MEDLINE=95034774; PubMed=7947749;
RA Proost P., Wuyts A., Lenaerts J.-P., van Damme J.;
RT "Purification, sequence analysis, and biological characterization of
RT a second bovine monocyte chemotactic protein-1 (Bo MCP-1B).";
RL Biochemistry 33:13406-13412(1994).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils. Augments monocyte anti-tumor activity. Also induces
CC the release of Gelatinase B. This protein can bind heparin.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC HSP; P13500; 1DOK.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR CYTOKINE; Chemotaxis; Signal; Inflammatory response; Glycoprotein;
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein;
FT NON_TER 1 1 BY SIMILARITY.
FT DISULFID 9 34 BY SIMILARITY.
FT DISULFID 10 50 BY SIMILARITY.
SQ SEQUENCE 74 AA; 8360 MW; FAF72B970EB16E3 CRC64;
Query Match 76.0%; Score 308; DB 1; Length 74;
Best Local Similarity 75.3%; Pred. No. 2.5e-29;
Matches 55; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 3 DAINAPVTCVYFNTRKISVQRLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62
Db 1 DAINSPVTCVYFNTRKISVQRLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
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DR EMBL; AF065936; AAF15386.1; -;
DR EMBL; AF065937; AAF15387.1; -;
DR EMBL; AF065938; AAF15388.1; -;
DR HSSP; P13500; 1DOL.
DR MGD; MGI:108224; Ccl12.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR CYTOKINE; Chemotaxis; Signal; Inflammatory response; Polymorphism.
KW CYTOKINE; Chemotaxis; Signal; Inflammatory response; Polymorphism.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 104 SMALL INDUCIBLE CYTOKINE A12.
FT DISULFID 33 58 BY SIMILARITY.
FT DISULFID 34 74 BY SIMILARITY.
FT VARIANT 94 104 QTFILPEPCLG -> RT (IN STRAIN SJL/J).
SQ SEQUENCE 104 AA; 8D102F4FAC3DBF CRC64;

Query Match 70.1%; Score 284; DB 1; Length 104;
Best Local Similarity 68.1%; Pred. No. 2.3e-26;
Matches 49; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 2 PDAINAPVTCCYNFTNKRISVORLASRYRITSKPKKAVIPKTVAKICADPKQKWQ 61
DB 24 PDVAVSTPVTCCYNVVKQIHVRKLKSYRITSQCPREAVIFRTILDKICADPKKWK 83

QY 62 DSWDHLDKOTOT 73
DB 84 NSINHLDKTSQT 95

RESULT 10
EOTA HUMAN STANDARD; PRT; 97 AA.
ID EOTA_HUMAN STANDARD; PRT; 97 AA.
AC P51671; P50877; Q92490; Q92491;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil
DE chemotactic protein).
GN CCL11 OR SCY11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96181758; PubMed=8597956;
RA Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
RA Luster A.D.;
RT "Human eotaxin is a specific chemoattractant for eosinophil cells and
RT provides a new mechanism to explain tissue eosinophilia.";
RL Nat. Med. 2:449-456(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96189937; PubMed=8609214;
RA Ponath P.D., Qin S., Ringler D.J., Clark-Lewis I., Wang J., Kassam N.,
RA Smith H., Shi X., Gonzalo J.A., Newman W., Gutierrez-Ramos J.C.,
RA Mackay C.R.;
RT "Cloning of the human eosinophil chemoattractant, eotaxin. Expression,
RT receptor binding, and functional properties suggest a mechanism for
RT the selective recruitment of eosinophils.";
RL J. Clin. Invest. 97:604-612(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Small intestine;
RA Kitaura M., Nakajima T., Imai T., Harada S., Combadiere C.,
RA Tiffany H.L., Murphy P.M., Yoshie O.;
RT "Molecular cloning of human eotaxin, an eosinophil-selective CC
RT chemokine, and identification of a specific eosinophil eotaxin
RT receptor, CC chemokine receptor 3.";
RL J. Biol. Chem. 271:7725-7730(1996).

RESULT 9

SY12_MOUSE STANDARD; PRT; 104 AA.
AC Q62401; Q9QYD6;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Small inducible cytokine A12 precursor (CCL12) (Monocyte chemotactic
DE protein 5) (MCP-5) (MCP-1 related chemokine).
GN CCL12 OR SCY12 OR MCP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079149; PubMed=8920881;
RA Jia G.-Q., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C.,
RA Werstlich B.X., Gutierrez-Ramos J.C.;
RT "Distinct expression and function of the novel mouse chemokine
RT monocyte chemotactic protein-5 in lung allergic inflammation.";
RL J. Exp. Med. 184:1939-1951(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97149436; PubMed=8996246;
RA Sarafi M.N., Garcia-Zepeda E.A., McLean J.A., Charo I.F., Luster A.D.;
RT "Murine monocyte chemoattractant protein (MCP)-5: a novel CC
RT chemokine that is a structural and functional homologue of human
RT MCP-1.";
RL J. Exp. Med. 185:99-109(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=B10.S/J, BALB/c, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scy1 (TCA-3), Scy12
RT (monocyte chemoattractant protein (MCP)-1), and Scy12 (MCP-5) are
RT candidates for eae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
CC -!- FUNCTION: Chemotactic factor that attracts eosinophils, monocytes,
CC and lymphocytes but not neutrophils. Potent monocyte active
CC chemokine that signals through CCR2. Involved in allergic
CC inflammation and the host response to pathogens and may play a
CC pivotal role during early stages of allergic lung inflammation.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- TISSUE SPECIFICITY: Predominantly expressed in the lymph nodes and
CC thymus. Also found in the salivary glands containing lymph nodes,
CC breast, heart, lung, brain, small intestine, kidney and colon.
CC -!- INDUCTION: By interferon gamma and lipopolysaccharides (LPS).
CC -!- POLYMORPHISM: The polymorphism in strain SJL/J may be associated
CC with severity of clinical symptoms of experimental allergic
CC encephalomyelitis, an animal model of multiple sclerosis, and
CC susceptibility to the monophasic remitting/nonrelapsing form of
CC the disease.
CC -!- SIMILARITY: Belongs to the interleukin 6 (chemokine CC) family.
CC
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DR EMBL; U50712; AAB50053.1; -;
DR EMBL; U66670; AAB49424.1; -;
DR EMBL; AF065934; AAF15384.1; -;
DR EMBL; AF065935; AAF15385.1; -;


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CC
CC EMBL; X99886; CAA68168.1; ALT_INIT.
CC EMBL; Y10802; CAA71760.1; -.
CC EMBL; Y16645; CAA76341.1; -.
CC PIR; JC5295; JC5295.
CC PDB; 1ESR; 06-DEC-00.
CC Genew; HGNC:10635; CCL8.
CC MIM; 602283; -.
CC GO; GO:0008009; P:chemokine activity; TAS.
CC GO; GO:0004871; P:signal transducer activity; TAS.
CC GO; GO:0006816; P:calcium ion transport; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0006887; P:exocytosis; TAS.
CC GO; GO:0009615; P:response to viruses; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR000827; CC:chemokine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
CC Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
CC Polymorphism; Pyrrolidone carboxylic acid; 3D-structure.
CC SIGNAL 1 23 PROBABLE.
CC CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A8.
CC MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
CC DISULFID 34 59 BY SIMILARITY.
CC DISULFID 35 75 BY SIMILARITY.
CC VARIANT 63 69 K -> Q.
CC FT FT FT /FTID-VAR 001633.
CC FT FT FT /FTID-VAR 9D67976B59422F2A CRC64;
CC SQ SEQUENCE 99 AA; 11246 MW; 9D67976B59422F2A CRC64;
Query Match .662%; Score 268; DB 1; Length 99;
Best Local Similarity 62.7%; Pred.No.1.6e-24;
Matches 47; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
Qy 1 QPDAINAPVTCVCYFNFRKISVORLASRYRIITSSKPKGKAVIEKTIKVAKEICADPKQKW 60
Db 24 QPDSVSIPITCCFCNVNIRKIPIQRLESYTRIINIQCPKGAIVPTKRGKEVCADPKERWV 83
Qy 61 QDSMDHLDKQTQPK 75
Db 84 RDSMKHLDFQMLK 98
RESULT 12
SY08_PIG ID_SY08_PIG STANDARD; PRT; 99 AA.
AC P49873;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
DE CCL8 OR SCYA8 OR MCP2.
DE OS scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95091716; PubMed=7999015;
RA Hosang K.K., Knoke I.I., Klaudiny J.J., Wempe F.F., Wuttke W.W.,
RA Schell K.K.,
RA "Porcine luteal cells express monocyte chemoattractant protein-2
-----

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RT (MCP-2): analysis by cDNA cloning and northern analysis.";
 RL Biochem. Biophys. Res. Commun. 205:148-153(1994).
 CC -!- FUNCTION: Chemotactic factor that attracts monocytes. This protein
 CC can bind heparin.
 CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
 CC -----
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 CC -----
 DR EMBL; Z48480; CAA88371.1; -;
 DR PIR; JC2417; JC2417.
 DR HSSP; P51671; 1E0T.
 DR InterPro: IPR000827; CC_chemokine_sml.
 DR InterPro: IPR001811; Chemokine_IL6.
 DR Pfam: PF00048; IL6; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 DR Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
 KW Pyrolidone carboxylic acid.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A8.
 FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT DISULFID 34 59 BY SIMILARITY.
 FT DISULFID 35 75 BY SIMILARITY.
 SQ SEQUENCE 99 AA; 10903 MW; D3DAA0F7A964CDB1 CRC64;
 Query Match 64.4%; Score 261; DB 1; Length 99;
 Best Local Similarity 60.0%; Pred. No. 1.1e-23;
 Matches 45; Conservative 16; Mismatches 14; Indels 0; Gaps 0;
 QY 1 OPDAINAPVTCYCNFTNRKISVORLASVRRITSSKCPKEAVIEKTIIVAKETICADPKQKW 60
 Db 24 QPDSVSIETCCFLVNGKIFPKLESYTRINSCQPOEAVIFKTKADKEVCADPQQKW 83
 QY 61 QSDMDHLKQQTTPK 75
 Db 84 QNSMKLLDQKSQTPK 98
 RESULT 13
 SV13_HUMAN
 ID SV13_HUMAN STANDARD; PRT; 98 AA.
 AC Q99616; O95689;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Small inducible cytokine A13 precursor (CC13) (Monocyte chemotactic
 DE protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CX-beta-10)
 DE (NCC-1).
 DE CCL13 OR SCYA13 OR MCP4 OR NCC1.
 GN Homo sapiens (Human).
 OS
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97113354; PubMed=8955214;
 RA Garcia-Zepeda E.A., Combadiere C., Rothenberg M.E., Sarafi M.N.,
 RA Lavigne P., Hamid A.Q., Murphy P.M., Luster A.D.;
 RT "Human monocyte chemoattractant protein (MCP)-4 is a novel CC
 RT chemokine with activities on monocytes, eosinophils, and basophils
 RT induced in allergic and nonallergic inflammation that signals through
 RT the CC chemokine receptors (CCR)-2 and -3.";
 RL J. Immunol. 157:5613-5626(1996).
 RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
 RC TISSUE=Fetal;
 RX MEDLINE=96235049; PubMed=8643349;
 RA Ugucioni M., Loetscher P., Forssmann U., Dewald B., Li H., Lima S.H.,
 RA Li Y., Kreider B., Garotta G., Thelen M., Baggiolini M.;
 RT "Monocyte chemotactic protein 4 (MCP-4), a novel structural and
 RT functional analogue of MCP-3 and eotaxin.";
 RL J. Exp. Med. 183:2379-2384(1996).
 RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
 RC TISSUE=Fetal;
 RX MEDLINE=97341179; PubMed=9195948;
 RA Berkhout T.A., Sarau H.M., Moores K., White J.R., Elshourbagy N.,
 RA Appelbaum E., Reape T.J., Brawner M., Makwana J., Foley J.J.,
 RA Schmidt D.B., Imburgia C., Macnulty D., Matthews J., O'Donnell K.,
 RA O'Shannessy D., Scott M., Groot P.H.E., Macphee C.;
 RT "Cloning, in vitro expression, and functional characterization of a
 RT novel human CC chemokine of the monocyte chemotactic protein (MCP)
 RT family (MCP-4) that binds and signals through the CC chemokine
 RT receptor 2B.";
 RL J. Biol. Chem. 272:16404-16413(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC Dante M., Gibson A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97213770; PubMed=9060459;
 RA Godiska R., Chantray D., Raport C.J., Schweickart V.L., Trong H.L.,
 RA Gray P.W.;
 RT "Monocyte chemotactic protein-4: tissue-specific expression and
 RT signaling through CC chemokine receptor-2.";
 RL J. Leukoc. Biol. 61:353-360(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=99160888; PubMed=10049733;
 RA Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,
 RA Bartels J.;
 RT "Genomic organization, sequence analysis and transcriptional
 RT regulation of the human MCP-4 chemokine gene (SCYA13) in dermal
 RT fibroblasts: a comparison to other eosinophilic beta-chemokines.";
 RL Biochem. Biophys. Res. Commun. 255:470-476(1999).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]

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OM protein - protein search, using sw model

Run on: August 30, 2004, 16:59:28 ; Search time 115 Seconds
(without alignments)
208.516 Million cell updates/sec

Title: 07330446.FEP

Perfect score: 405

Sequence: 1 gpdainapvcocynftnrki.....qkwvqdsmdhldkgtqtpkt 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:**

1: sp_archaea:**

2: sp_bacteria:**

3: sp_fungi:**

4: sp_human:**

5: sp_invertebrate:**

6: sp_mammal:**

7: sp_mhc:**

8: sp_organelle:**

9: sp_phage:**

10: sp_plant:**

11: sp_rodent:**

12: sp_virus:**

13: sp_vertebrate:**

14: sp_unclassified:**

15: sp_rvirus:**

16: sp_bacteriap:**

17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	330	81.5	99	6	Q9TTQ3
2	297	73.3	109	6	Q865F3
3	287	70.9	109	4	Q727Q8
4	277	68.4	99	6	Q8MKC8
5	274	67.7	99	6	Q865F4
6	271	66.9	99	6	Q8HYQ0
7	261	64.4	97	6	Q8MI77
8	261	64.4	97	6	Q8HXZ5
9	260	64.2	150	11	Q8CGM5
10	252	62.2	100	6	Q9TTQ4
11	249	61.5	97	11	Q9Z318
12	247	61.0	100	6	Q8MDP5
13	235	58.0	97	6	Q9TTQ6
14	211	52.1	81	6	Q9TTQ2
15	190.5	47.0	75	6	Q9TTQ1
16	183	45.2	62	4	Q95690

ALIGNMENTS

RESULT 1

Q9TTQ3 PRELIMINARY; PRT; 99 AA.

```

17 177 43.7 106 11 Q9Z292
18 173 42.7 65 11 Q7TMS1
19 156 38.5 44 6 Q9BG83
20 154 38.0 119 11 Q8K477
21 149.5 36.9 92 6 Q8MI76
22 143.5 35.4 92 11 Q91ZL0
23 139.5 34.4 80 4 Q14745
24 138.5 34.2 92 6 Q8HYQ2
25 137 33.8 91 13 Q8QGS7
26 136 33.6 89 11 Q8OX14
27 135.5 33.5 56 6 Q8HYN4
28 135.5 33.5 90 13 Q9PWA6
29 134.5 33.2 91 13 Q8QGS6
30 134.5 33.2 92 4 Q8NHW4
31 133.5 33.0 93 6 Q8SOA6
32 133.5 33.0 93 11 Q9ERE0
33 132.5 32.7 92 6 Q8HYQ3
34 130 32.1 131 6 Q8HYP5
35 128.5 31.7 91 13 Q8JIMS
36 128.5 31.7 91 13 Q8AV56
37 128.5 31.7 101 12 Q8TR57
38 128 31.6 395 11 Q8C9Y1
39 128 31.6 395 11 Q9IV44
40 127.5 31.5 91 13 Q8JIM4
41 126.5 31.2 85 11 Q8OXG5
42 124.5 30.7 99 6 Q95N01
43 120.5 29.8 97 13 Q57411
44 119 29.4 407 6 Q865F6
45 119 29.4 408 6 Q8HXZ1

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Q9TTQ3 PRELIMINARY; PRT; 99 AA.
AC Q9TTQ3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte chemoattractant protein-1 precursor.
GN MCP-1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21061912; PubMed=11044560;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).

Query Match 81.5%; Score 330; DB 6; Length 99;

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RT assignment to the C-C chemokine gene cluster on chromosome 17q11.2-
RT q12.2;
RL Genomics 21:403-408(1994).
DR EMBL; X72309; CABS9723.1; -.
SQ SEQUENCE 109 AA; 12356 MW; 69980669FOA2157D CRC64;

Query Match 70.9%; Score 287; DB 4; Length 109;
Best Local Similarity 72.0%; Pred. No. 6.4e-28;
Matches 54; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 34 QPDGINTSTTCYRINKIPKQRLSYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 93

QY 61 QDSMDHLDKQTQTPK 75
Db 94 QDFMKHLDKKTQTPK 108

RESULT 4
Q8MKC8 PRELIMINARY; PRT; 99 AA.
AC Q8MKC8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MCP-2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RT "Equus caballus monocyte chemoattractant protein-2 (mcp-2), complete
RT cds".
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506972; AAM34214.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR SWART; SM00199; SCY; 1.
SQ SEQUENCE 99 AA; 11028 MW; 94F5D8E540889228 CRC64;

Query Match 68.4%; Score 277; DB 6; Length 99;
Best Local Similarity 65.3%; Pred. No. 1e-26;
Matches 49; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDASIPVTCGVDVKPIQRVESYTRITSSQCSQEAIVFKTKVKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPK 75
Db 84 QDMKELDQSQTPK 98

RESULT 5
Q865F4 PRELIMINARY; PRT; 99 AA.
AC Q865F4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemoattractant protein-2.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Coleman G.D., Valli P.J.S., Clements J.E., Zink M.C.;
RT "Macaca nemestrina (Pig-tailed macaque) monocyte chemoattractant
RT protein-3 (MCP-3)".
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY206694; AAO52735.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC:chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 109 AA; 12346 MW; D031826233EC461A CRC64;

Query Match 73.3%; Score 297; DB 6; Length 109;
Best Local Similarity 73.3%; Pred. No. 3.6e-29;
Matches 55; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 34 QPDGINTSTTCYRINKIPKQRLSYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 93

QY 61 QDSMDHLDKQTQTPK 75
Db 94 QDFMKHLDKKTQTPK 108

RESULT 3
Q727Q8 PRELIMINARY; PRT; 109 AA.
AC Q727Q8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemotactic protein-3.
OS MCP-3.
ON Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94375065; PubMed=7916328;
RA Opdenakker G.M.M.;
RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
```

```
RT assignment to the C-C chemokine gene cluster on chromosome 17q11.2-
RT q12.2;
RL Genomics 21:403-408(1994).
DR EMBL; X72309; CABS9723.1; -.
SQ SEQUENCE 109 AA; 12356 MW; 69980669FOA2157D CRC64;

Query Match 70.9%; Score 287; DB 4; Length 109;
Best Local Similarity 72.0%; Pred. No. 6.4e-28;
Matches 54; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 34 QPDGINTSTTCYRINKIPKQRLSYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 93

QY 61 QDSMDHLDKQTQTPK 75
Db 94 QDFMKHLDKKTQTPK 108

RESULT 4
Q8MKC8 PRELIMINARY; PRT; 99 AA.
AC Q8MKC8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MCP-2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RT "Equus caballus monocyte chemoattractant protein-2 (mcp-2), complete
RT cds".
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506972; AAM34214.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR SWART; SM00199; SCY; 1.
SQ SEQUENCE 99 AA; 11028 MW; 94F5D8E540889228 CRC64;

Query Match 68.4%; Score 277; DB 6; Length 99;
Best Local Similarity 65.3%; Pred. No. 1e-26;
Matches 49; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDASIPVTCGVDVKPIQRVESYTRITSSQCSQEAIVFKTKVKEICADPKQKW 83

QY 61 QDSMDHLDKQTQTPK 75
Db 84 QDMKELDQSQTPK 98

RESULT 5
Q865F4 PRELIMINARY; PRT; 99 AA.
AC Q865F4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemoattractant protein-2.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Coleman G.D., Valli P.J.S., Clements J.E., Zink M.C.;
RT "Macaca nemestrina (Pig-tailed macaque) monocyte chemoattractant
RT protein-3 (MCP-3)".
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY206694; AAO52735.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC:chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 109 AA; 12346 MW; D031826233EC461A CRC64;

Query Match 73.3%; Score 297; DB 6; Length 109;
Best Local Similarity 73.3%; Pred. No. 3.6e-29;
Matches 55; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 34 QPDGINTSTTCYRINKIPKQRLSYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 93

QY 61 QDSMDHLDKQTQTPK 75
Db 94 QDFMKHLDKKTQTPK 108

RESULT 3
Q727Q8 PRELIMINARY; PRT; 109 AA.
AC Q727Q8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemotactic protein-3.
OS MCP-3.
ON Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94375065; PubMed=7916328;
RA Opdenakker G.M.M.;
RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
```

RA SEQUENCE FROM N.A.
 RP Coleman G.D., Clements J.E., Zink M.C.; MCP-2 (CC) chemokine."
 RT "Macaca nemestrina (pig-tailed macaque) MCP-2 (CC) chemokine."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY206693; AAO52734.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008009; P:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000827; CC:chemokine; IEA.
 DR InterPro; IPR001811; CC:chemokine; IEA.
 DR InterPro; IPR008097; Fractalkine.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR01721; FRCTALKINE.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
 SQ SEQUENCE 99 AA; 11283 MW; 9D6797974A88B9F7 CRC64;

Query Match 67.7%; Score 274; DB 6; Length 99;
 Best Local Similarity 62.7%; Pred. No. 2.4e-26;
 Matches 47; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKKQWV 60
 Db 24 QPDSVSIPTCCFNVINRKIPQRLQSYTRITNQCPEAVIFKTKMGKVCADPKKRW 83
 QY 61 QDSMDHLDKQTQTPK 75
 Db 84 RDSMKHLDQIFQNLK 98

RESULT 6

Q8HYQ0 PRELIMINARY; PRT; 99 AA.
 AC Q8HYQ0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DR Chemokine CC18/MCP-2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

SEQUENCE FROM N.A.

RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
 RT "Comprehensive cloning and sequencing reveals evolutionary
 conservation among all groups of rhesus macaque chemokines."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF449289; AAN76073.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008009; P:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000827; CC:chemokine; IEA.
 DR InterPro; IPR001811; CC:chemokine; IEA.
 DR InterPro; IPR008097; Fractalkine.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR01721; FRCTALKINE.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
 SQ SEQUENCE 99 AA; 11263 MW; 9D6797974A88B9F7 CRC64;

Query Match 66.9%; Score 271; DB 6; Length 99;
 Best Local Similarity 62.7%; Pred. No. 5.7e-26;
 Matches 47; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKKQWV 60
 Db 24 QPDSVSIPTCCFNVINRKIPQRLQSYTRITNQCPEAVIFKTKMGKVCADPKKRW 83
 QY 61 QDSMDHLDKQTQTPK 75

Db 84 RDSMKHLDQIFQNLK 98

RESULT 7

Q8MIT7 PRELIMINARY; PRT; 97 AA.
 AC Q8MIT7;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Eotaxin.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

SEQUENCE FROM N.A.

RA Zhang L., Soares M.P., Guan Y., Sirotina-Meisher A.,
 RA Matheravidathu S., Iliff S.A., Mudgett J.S., Springer M.S.,
 RA Daugherty B.L.;

RT "Molecular cloning of eotaxin/CCL11 and CCR3 from rhesus monkey.
 RT Functional expression and characterization of rhesus monkey CCR3 in
 RT murine Li-2 cells; Generation of antibodies against rhesus CCR3."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY049019; AAL13066.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008009; P:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000827; CC:chemokine; IEA.
 DR InterPro; IPR001811; CC:chemokine; IEA.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
 SQ SEQUENCE 97 AA; 10855 MW; 9BCA0FD6D95B02DD CRC64;

Query Match 64.4%; Score 261; DB 6; Length 97;
 Best Local Similarity 63.5%; Pred. No. 9.8e-25;
 Matches 47; Conservative 14; Mismatches 11; Indels 2; Gaps 1;

QY 2 PDRAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKKQWV 61
 Db 25 PDSV--ATTCCFTLNKKIPQLRLESYRRIISGKCPQKAVIFKTKLADICADPKKQWV 82
 QY 62 DSDMDHLDKQTQTPK 75

Db 83 DSMKYLDKSPKPK 96

RESULT 8

Q8HXZ5 PRELIMINARY; PRT; 97 AA.
 AC Q8HXZ5;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Chemokine CCL11/eotaxin.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

SEQUENCE FROM N.A.

RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
 RT "Comprehensive cloning and sequencing reveals evolutionary
 conservation among all groups of rhesus macaque chemokines."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF449270; AAN76074.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008009; P:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.

7

Query Match 61.5%; Score 249; DB 11; Length 97;
Best Local Similarity 63.2%; Pred. No. 3.1e-23;
Matches 48; Conservative 13; Mismatches 13; Indels 2; Gaps 2;
QY 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPDGWNIS-TCCKY-RSQIRVORLESYTRITSSKCPQWQAVIFKTKENREICADPKQKW 81
QY 61 QDSMDHLDKQTQTPKT 76
DB 82 QDSMKYIDKSKTPTKS 97
RESULT 12
Q9TTS6 PRELIMINARY; PRT; 100 AA.
AC Q9TTS6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemoattractant protein 2 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Weeling D.;
RT "Role of chemokines in respiratory syncytial virus infection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399641; AAK94451.1; -
DR HSSP; Q9Y258; IG28.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
FT NON TER 1
SQ SEQUENCE 100 AA; FID308AD924PCAF6 CRC64;
Query Match 61.0%; Score 247; DB 6; Length 100;
Best Local Similarity 56.0%; Pred. No. 5.6e-23;
Matches 42; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 25 QPDSVSTITCFSVINGKIFPKLDSYTRITNSQCPQWQAVIFKTKADRDVADPKQKW 84
QY 61 QDSMDHLDKQTQTPK 75
DB 85 QTSIRLLDQKSTPK 99
RESULT 13
Q9TTS6 PRELIMINARY; PRT; 97 AA.
AC Q9TTS6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Eotaxin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

Vogel B., Klinder A., Aust G.;
"Molecular cloning of bovine eotaxin mRNA."
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132003; CAB61617.1; -
DR HSSP; P51671; IEOT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 97 AA; 965F23E1DDDB743 CRC64;
Query Match 58.0%; Score 235; DB 6; Length 97;
Best Local Similarity 55.3%; Pred. No. 1.7e-21;
Matches 42; Conservative 20; Mismatches 12; Indels 2; Gaps 1;
QY 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 24 QPASI--PTICFNMSKKKISIQRLSQSYRRIITSSKCPQWQAVIFKTKQNKKKICVDPKQKW 81
QY 61 QDSMDHLDKQTQTPKT 76
DB 82 QNAMEYLNQSKTILKS 97
RESULT 14
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ID Q9TTQ2
AC Q9TTQ2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte chemoattractant protein-2 precursor (Fragment).
GN MCP-2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21061912; PubMed=11044560;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and induction by IL-4 in dermal fibroblasts."
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
DR EMBL; AJ251190; CAB61626.1; -
DR HSSP; P13500; IDOK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL
FT CHAIN 24 >81 BY SIMILARITY.
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SQ SEQUENCE 81 AA; 8858 MW; A34ADE103C386B0F CRC64;
Query Match 52.1%; Score 211; DB 6; Length 81;
Best Local Similarity 65.5%; Pred. No. 1.4e-18;
Matches 38; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 58
DB 24 QPDASVTPVTCFQVWKKVPIQRLSEYTRITSSQSQEAVIFKTKVDEICADPKKK 81
RESULT 15

Q9TTQ1
 ID Q9TTQ1 PRELIMINARY; PRT; 75 AA.
 AC Q9TTQ1;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Monocyte chemoattractant protein-4 precursor (Fragment).
 GN MCP-4.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=21061912; PubMed=1104560;
 RX Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
 RA Collins M.E.;
 RT "Cloning of equine chemokines sotaxin, monocyte chemoattractant
 protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
 induction by IL-4 in dermal fibroblasts";
 RL Vet. Immunol. Immunopathol. 76:283-298(2000).
 DR EMBL; A0251191; CAB61627.1; -.
 DR HSSP; P51671; LEOT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008009; F:chemokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
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 FT NON_TER 1
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 Matches 34; Conservative 14; Mismatches 9; Indels 1; Gaps 1;

QY 1 OPDAINPVTCYNTNEKISVORLASVERITSSKCPKEAVIETIVAKEICADPKOK 58
 Db 19 QFDALSALTACCFKFNKMPQLRYSY-RITGSCPOEAVIFRTKLAKDVCAADPKKK 75

Search completed: August 30, 2004, 17:07:19
 Job time : 119 secs

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:12 ; Search time 1389 Seconds
(without alignments)
7114.623 Million cell updates/sec

Title: 07330446
Perfect score: 228
Sequence: 1 cagccgatgcaatcaatgc.....aaacccaaactccgaagact 228

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb.ba.*
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- 3: gb.in.*
- 4: gb.om.*
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- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
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- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	228	100.0	228	6	BD102671	BD102671 Compositi
2	228	100.0	228	6	BD137507	BD137507 Preventiv
3	228	100.0	300	6	BD168034	BD168034 Novel hep
4	228	100.0	300	6	BD177097	BD177097 Prophylac
5	228	100.0	300	12	BT007880	BT007880 Synthetic D
6	228	100.0	418	6	E05615	E05615 Synthetic D
7	228	100.0	554	6	E05599	E05599 CDNA encodi
8	228	100.0	647	6	AX698741	AX698741 Sequence
9	228	100.0	725	6	AR337874	AR337874 Sequence
10	228	100.0	725	6	AR380799	AR380799 Sequence
11	228	100.0	725	6	AX774742	AX774742 Sequence
12	228	100.0	725	9	HSMCP1	X14768 H.sapiens m
13	228	100.0	739	6	AX577974	AX577974 Sequence
14	228	100.0	739	9	S71513	S71513 monocyte ch
15	228	100.0	741	6	A17786	A17786 MCP-1 mRNA.
16	228	100.0	741	6	AR094465	AR094465 Sequence
17	228	100.0	741	6	E05611	E05611 CDNA encodi
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21	228	100.0	978	6	AX838969	AX838969 Sequence
22	228	100.0	978	6	BD222013	BD222013 Method an
23	228	100.0	984	6	AX838970	AX838970 Sequence
24	228	100.0	984	6	BD222014	BD222014 Method an
25	228	100.0	999	6	AX838971	AX838971 Sequence
26	228	100.0	999	6	BD222015	BD222015 Method an
27	227.6	99.8	1712	6	AR352699	AR352699 Sequence
28	227.6	99.8	1712	6	BD195644	BD195644 70 human
29	227.6	99.8	1822	6	AR352698	AR352698 Sequence
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34	226.4	99.3	356	6	BD058323	BD058323 Secreted
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44	211.2	92.6	361	6	BD058318	BD058318 Secreted
45	205.2	90.0	279	6	BD168033	BD168033 Novel hep

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Composition for treating or preventing primary pulmonary
 228 bp DNA linear PAT 27-AUG-2002
 hypertension.
ACCESSION BD102671
VERSION BD102671.1 GI:22648245
KEYWORDS WO 0189582-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS Bgashira,K., Yonemitsu,Y., Sueishi,K., Ikeda,Y. and Inada,Y.
TITLE Composition for treating or preventing primary pulmonary

JOURNAL Patent: WO 0189582-A 1 29-NOV-2001;
TAKEDA CHEMICAL INDUSTRIES LTD KENSUKE EGASHIRA, YOSHIKAZU
YONEMITSU, KATSUO SUEISHI, YASUHIRO IKEDA, YOSHIYUKI INADA
COMMENT OS Homo sapiens (human)
PN WO 0189582-A/1
PD 29-NOV-2001
PF 25-MAY-2001 WO 2001JP004381
PR 26-MAY-2000 JP OOP 161145
PI KENSUKE EGASHIRA, YOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUHIRO
IKEDA,
PI YOSHIYUKI INADA
PC A61K48/00, A61K39/395, A61K31/711, A61P11/00, A61P9/12
CC Composition for treating or preventing primary pulmonary CC
hypertension
FH Key Location/Qualifiers
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FT Location/Qualifiers
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DB 121 GTGATCTTCAGACCAATGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGTT 180
QY 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228
DB 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228

RESULT 3
BD168034
LOCUS
Novel hepatic disease agent.
DEFINITION
ACCESSION BD168034
VERSION BD168034.1 GI:27873846
KEYWORDS WO 0230464-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 300)
AUTHORS Egashira, K., Takeshita, A., Koyanagi, M., Nakamura, M. and Nishida, K.
TITLE Novel hepatic disease agent
JOURNAL Patent: WO 0230464-A 2 18-APR-2002;
KENSUKE EGASHIRA, DAIICHI PHARMACEUTICAL CO LTD, AKIRA TAKESHITA,
MASAMICHI KOYANAGI, MAKOTO NAKAMURA, KENICHI NISHIDA
COMMENT OS Homo sapiens (human)
PN WO 0230464-A/2
PD 18-APR-2002
PF 18-SEP-2001 WO 2001JP008552
PR 11-OCT-2000 JP OOP 310604
PI KENSUKE EGASHIRA, AKIRA TAKESHITA, MASAMICHI KOYANAGI, MAKOTO NAKAMURA,
KENICHI NISHIDA
PC A61K45/00, A61K48/00, A61P43/00, A61P1/16
CC Novel hepatic disease agent
FH Key Location/Qualifiers
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FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.3e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TCAGTCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 61 TCAGTCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
QY 121 GTGATCTTCAGACCAATGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGTT 180
DB 121 GTGATCTTCAGACCAATGTGCGCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGTT 180
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DB 181 CAGGATTCATGGACCACTGGACCAAGCAAAACCCAACTCCGAAGACT 228

RESULT 2
BD137507
LOCUS
Preventive or remedy for pulmonary hypertension.
DEFINITION
ACCESSION BD137507
VERSION BD137507.1 GI:23232452
KEYWORDS JP 2002047203-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS Egashira, K., Yonemitsu, Y., Sueishi, K., Ikeda, Y. and Inada, Y.
TITLE Preventive or remedy for pulmonary hypertension
JOURNAL Patent: JP 2002047203-A 1 12-FEB-2002;
KENSUKE EGASHIRA, TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2002047203-A/1
PD 12-FEB-2002
PF 25-MAY-2001 JP 2001156252
PR 25-MAY-2001 JP 2001156252
PI KENSUKE EGASHIRA, YOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUHIRO
IKEDA,
PI YOSHIYUKI INADA
PC A61K38/00, A61K31/7085, A61K39/395, A61K39/395, A61K48/00, A61P9/12,
PC A61P11/00, C07K14/52, C07K16/24//C12N15/09, A61K37/02, C12N15/00
CC Preventive or remedy for pulmonary hypertension FH Key

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Db	130	TCAGTGCAGAGGCTCGCGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT	189
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Db	190	GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTCTGACCCCAAGCAGAGTGGGTT	249
Qy	181	CAGGATTCATGGACCACTGGCAAGCAACCACTCGAAGACT	228
Db	250	CAGGATTCATGGACCACTGGCAAGCAACCACTCGAAGACT	297
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LOCUS	BD177097	300 bp	DNA linear PAT 16-APR-2003
DEFINITION	Prophylactic and/or remedy for vascular restenosis.		
ACCESSION	BD177097		
VERSION	BD177097.1	GI:30014357	
KEYWORDS	JP 2002284698-A/2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 300)		
TITLE	Prophylactic and/or remedy for vascular restenosis		
JOURNAL	Patent: JP 2002284698-A 2 03-OCT-2002;		
COMMENT	KENSUKE EGASHIRA, DAIICHI PHARMACEUTICAL CO LTD		
	OS Homo sapiens (human)		
	PN JP 2002284698-A/2		
	PD 03-OCT-2002		
	PF 23-MAR-2001 JP 2001085073		
	PI KENSUKE EGASHIRA, AKIRA TAKESHITA		
	PC		
	A61K45/00, A61K31/711, A61K35/76, A61K38/00, A61K39/395, A61K39/395, PC		
	A61K48/00,		
	PC A61P9/10, A61P9/10//C12N15/09, A61K37/02, C12N15/00 CC		
	Prophylactic and/or remedy for vascular restenosis FH Key		
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Best Local Similarity	100.0%;	Pred. No. 7.3e-57;	Mismatches 0; Indels 0; Gaps 0;
Matches	228; Conservative	0;	
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Qy	61	TCAGTGCAGAGGCTCGCGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT	120
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Db	250	CAGGATTCATGGACCACTGGCAAGCAACCACTCGAAGACT	297
RESULT 5			
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LOCUS	BD177097	300 bp	mRNA linear SYN 13-MAY-2003
DEFINITION	Synthetic construct Homo sapiens chemokine (C-C motif) ligand 2		
ACCESSION	BT007880		
VERSION	BT007880.1	GI:30584598	
KEYWORDS	FLI_CDNA.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 300)		
AUTHORS	Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.		
TITLE	Cloning of human full-length CDSs in BD Creator(TM) System Donor		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 300)		
AUTHORS	Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow		
COMMENT	Circle, Palo Alto, CA 94303, USA		
	This CDS clone is a part of a collection of human full length		
	expression clones generated by BD Biosciences Clontech and the		
	Harvard Institute of Proteomics. Each CDS has been cloned in two		
	forms: with and without stop-codon (to allow fusion with C-terminal		
	tag). The CDS has been directionally cloned using BD In-Fusion(TM)		
	cloning system between the SalI and HindIII sites of the pDNR-DUAL		
	vector. Additional sequences in the clone: 'ACC' after SalI site		
	and before 'ATG' to provide Kozak consensus sequence; 'GG' after		
	last codon and before HindIII site to maintain reading frame.		
	Clone distribution: http://bioinfo.clontech.com/orfclones.		
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Best Local Similarity	100.0%;	Pred. No. 7.3e-57;	Mismatches 0; Indels 0; Gaps 0;
Matches	228; Conservative	0;	
Qy	1	CAGCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATTAACTTCAACCAATAGGAAGATC	60
Db	70	CAGCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATTAACTTCAACCAATAGGAAGATC	129
Qy	61	TCAGTGCAGAGGCTCGCGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT	120
Db	130	TCAGTGCAGAGGCTCGCGAGCTATAGAAAGATACACAGCAGCAAGTGTCCCAAGAAGCT	189
Qy	121	GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTCTGACCCCAAGCAGAGTGGGTT	180
Db	190	GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTCTGACCCCAAGCAGAGTGGGTT	249
Qy	181	CAGGATTCATGGACCACTGGCAAGCAACCACTCGAAGACT	228

Db 250 CAGGATTCATGGACCACTGGAGCAAGCAACCACTCGAAGACT 297

RESULT 6
LOCUS E05615
DEFINITION Synthetic DNA.
ACCESSION E05615
VERSION E05615.1 GI:2173802
KEYWORDS JP 1993260987-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 (bases 1 to 418)
Yamagishi,J., Matsuo,T., Fukui,J. and Yamada,M.
PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYPEPTIDE AND MICROBIAL STRAIN PRODUCING THE POLYPEPTIDE
Patent: JP 1993260987-A 19 12-OCT-1993;
DAINIPPON PHARMACEUT CO LTD

JOURNAL
OS Artificial Gene
OC Artificial sequence; Genes.
PN JP 1993260987-A/19
PD 12-OCT-1993
PF 28-APR-1992 JP 1992136213
PI 09-MAY-1991 JP 91P 135950
PI YAMAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI YAMADA MASAAKI

PC C12P21/02,C12N1/21//C12N15/12,(C12P21/02,C12R1:19),(C12N1/21,
C12R1:19);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC anti-sense: No.

FEATURES
source
Location/Qualifiers
1..418
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 228; DB 6; Length 418;
Best Local Similarity 100.0%; Pred. No. 7.4e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATCTTACCAATAGGAAGTC 60
DB 150 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATCTTACCAATAGGAAGTC 209
QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCAACGAGCAAGTGTCCCAAGAAGCT 120
DB 210 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCAACGAGCAAGTGTCCCAAGAAGCT 269
QY 121 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 270 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 329
QY 181 CAGGATTCATGGACCACTGGACAAGCAACCACTCGAAGACT 228
DB 330 CAGGATTCATGGACCACTGGACAAGCAACCACTCGAAGACT 377

RESULT 7
LOCUS E05599
DEFINITION cDNA encoding monocyte chemotactic factor.
ACCESSION E05599
VERSION E05599.1 GI:2173786
KEYWORDS JP 1993260987-A/3.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1 (bases 1 to 554)

Yamagishi,J., Matsuo,T., Fukui,J. and Yamada,M.
PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYPEPTIDE AND MICROBIAL STRAIN PRODUCING THE POLYPEPTIDE
Patent: JP 1993260987-A 3 12-OCT-1993;
DAINIPPON PHARMACEUT CO LTD

COMMENT
PN JP 1993260987-A/3
PD 12-OCT-1993
PF 28-APR-1992 JP 1992136213
PI 09-MAY-1991 JP 91P 135950
PI YAMAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI YAMADA MASAAKI

PC C12P21/02,C12N1/21//C12N15/12,(C12P21/02,C12R1:19),(C12N1/21,
C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC anti-sense: No;
FH Key
FT Location/Qualifiers
5'UTR 1..39
RBS 22..29
FT mat_peptide 40..267
FT /product='monocyte chemotactic factor' FT
CDS 40..270
FT /product='monocyte chemotactic factor' FT
3'UTR 271..554.
Location/Qualifiers
1..554
/organism="Escherichia coli"
/mol_type="genomic RNA"
/db_xref="taxon:562"

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source
Location/Qualifiers
1..554
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/mol_type="genomic RNA"
/db_xref="taxon:562"

ORIGIN
Query Match 100.0%; Score 228; DB 6; Length 554;
Best Local Similarity 100.0%; Pred. No. 7.4e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATCTTACCAATAGGAAGTC 60
DB 40 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATCTTACCAATAGGAAGTC 99
QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCAACGAGCAAGTGTCCCAAGAAGCT 120
DB 100 TCAGTGCAGAGCTCGCGAGCTATAGAGAATCAACGAGCAAGTGTCCCAAGAAGCT 159
QY 121 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 160 GTGATCTTCAAGACCATTTGGCCAGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 219
QY 181 CAGGATTCATGGACCACTGGACAAGCAACCACTCGAAGACT 228
DB 220 CAGGATTCATGGACCACTGGACAAGCAACCACTCGAAGACT 267

RESULT 8
LOCUS AX698741
DEFINITION Sequence 72 from Patent WO02063030.
ACCESSION AX698741
VERSION AX698741.1 GI:29499529
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1
Lyanichev,V., Skrzypczynski,Z., Allawi,H.T., Wayland,S.R., Takova,T. and Neri,B.P.
Charge tags and separation of nucleic acid molecules
Patent: WO 02063030-A 72 15-AUG-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
Location/Qualifiers
1..647
/organism="synthetic construct"

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/mol_type="unassigned RNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 228; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 60
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Db 70 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 129

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 120
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Db 130 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 189

QY 121 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 180
   |||
Db 190 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 249

QY 181 CAGGATTCATGACCACTGCAACGACAAACCCAACTCCGAAGACT 228
   |||
Db 250 CAGGATTCATGACCACTGCAACGACAAACCCAACTCCGAAGACT 297

RESULT 9
AR337874
LOCUS      AR337874      725 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 3 from patent US 6569418.
ACCESSION AR337874
VERSION    AR337874.1 GI:33724486
KEYWORDS   Location/Qualifiers
SOURCE     1..725
           /organism="unknown"
           /mol_type="genomic DNA"

Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 725)
AUTHORS   Garzino-Demo,A. and Devico,A.L.
TITLE     Immuno-modulating effects of chemokines in DNA vaccination
JOURNAL   Patent: US 6569418-A 3 27-MAY-2003;
FEATURES   Location/Qualifiers
           1..725
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 228; DB 6; Length 725;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 60
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Db 70 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 129

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 120
   |||
Db 130 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 189

QY 121 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 180
   |||
Db 190 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 249

QY 181 CAGGATTCATGACCACTGCAACGACAAACCCAACTCCGAAGACT 228
   |||
Db 250 CAGGATTCATGACCACTGCAACGACAAACCCAACTCCGAAGACT 297

RESULT 10
AR380799
LOCUS      AR380799      725 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 1344 from patent US 6607879.
ACCESSION AR380799
VERSION    AR380799.1 GI:40088433
KEYWORDS   Location/Qualifiers
SOURCE     1..725
           /organism="unknown"
           /mol_type="genomic DNA"

Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 725)
AUTHORS   Raponi,M.
TITLE     Methods for assessing and treating leukemia
JOURNAL   Patent: WO 03038129-A 58 08-MAY-2003;
           Ortho-Clinical Diagnostics, Inc. (US)
FEATURES   Location/Qualifiers
           1..725
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 228; DB 6; Length 725;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 60
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Db 123 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 120
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Db 183 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 242

QY 121 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 180
   |||
Db 243 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 302

RESULT 11
AR337874
LOCUS      AR337874      725 bp      DNA      linear      PAT 09-JUL-2003
DEFINITION Sequence 58 from Patent WO03038129.
ACCESSION AR337874
VERSION    AR337874.1 GI:32486258
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           Raponi,M.
           Methods for assessing and treating leukemia
           Patent: WO 03038129-A 58 08-MAY-2003;
           Ortho-Clinical Diagnostics, Inc. (US)
FEATURES   Location/Qualifiers
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           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 60
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Db 123 CAGCCAGATGCAATCAATGCCCCAGTCCACCTGCTGTTTAACTTCACCAATAGGAAGATC 182

QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 120
   |||
Db 183 TCAGTGCAGAGGCTCGGAGCTATAGAGATCAACGACGACGAGTGTCCCAAGAGCT 242

QY 121 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 180
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Db 243 GTGATCTTCAAGACCAATTTGGCCCAAGAGATCTGTGTCACCCCAAGCAGAAAGTGGTT 302

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181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228
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 Db 303 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 350

RESULT 12
 HSMCP1
 LOCUS
 DEFINITION H.sapiens mRNA for monocyte chemoattractant protein 1 (MCP-1). PRI 03-APR-1995
 ACCESSION X14768
 VERSION X14768.1 GI:34513
 KEYWORDS monocyte chemoattractant protein 1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 725)
 AUTHORS Yoshimura, T., Yuhki, N., Moore, S.K., Appella, E., Lerman, M.I. and Leonard, E.J.
 TITLE Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JE
 JOURNAL FEBS Lett. 244 (2), 487-493 (1989)
 MEDLINE 89153605
 PUBMED 2465924
 COMMENT ZAP11.
 FEATURES
 source Location/Qualifiers
 1..725
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_lines="U105MG"
 /cell_type="glioma cells"
 /clone_lib="lambda"
 54..353
 /codon_start=1
 /product="monocyte chemoattractant preprotein"
 /protein_id="CAA32876.1"
 /db_xref="GI:34514"
 /db_xref="GOA:P13500"
 /db_xref="SWISS-PROT:P13500"
 /translation="MKVSAALLCLLLAATFIPQGLAAPPDAINAPVTCVNFNTRKIS
 VQLASVRRITSSKCPKEAVIFKTVAKEICADPKQKWDMDHLDKQTQPKT"
 54..122
 /note="signal peptide (AA -23 to -1)"
 123..350
 /product="MCP-1 (AA 1 - 76)"
 162..170
 /note="pot. N-linked glycosylation site"
 707..712
 /note="pot. polyA signal"
 725
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 7.5e-57;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATACTTCCCAATAGGAAGATC 60
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 Db 123 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATACTTCCCAATAGGAAGATC 182
 |||||
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAAGATCACCAGCAAGTGTCCCAAGAAAGCT 120
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 Db 183 TCAGTGCAGAGCTCGCGAGCTATAGAAGATCACCAGCAAGTGTCCCAAGAAAGCT 242
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 |||||
 QY 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228

Db 303 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 350
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 RESULT 13
 AX577974
 LOCUS
 DEFINITION Sequence 96 from Patent WO02081745.
 ACCESSION AX577974
 VERSION AX577974.1 GI:27647182
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Garcia, T., roman Roman, S., Baron, R., Call, K., Theilhaber, J., Connolly, T., Jackson, A., Bushnell, S.E. and Rawadi, G.
 TITLE Genes involved in osteogenesis and methods of use
 JOURNAL Patent: WO 02081745-A 96 17-OCT-2002;
 Aventis Pharma S.A. (FR)
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

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 QY 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTATACTTCCCAATAGGAAGATC 60
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 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAAGATCACCAGCAAGTGTCCCAAGAAAGCT 120
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 Db 183 TCAGTGCAGAGCTCGCGAGCTATAGAAGATCACCAGCAAGTGTCCCAAGAAAGCT 242
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 QY 121 GTGATCTTCAGACCATTTGGCCCAAGAGATCTGTGTGACCCCAAGCAGAGTGGGTT 180
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 QY 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228
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 Db 303 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 350
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RESULT 14
 S71513
 LOCUS
 DEFINITION monocyte chemoattractant protein-1 [human, mRNA, 739 nt].
 ACCESSION S71513
 VERSION S71513.1 GI:240867
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 739)
 AUTHORS Yoshimura, T. and Leonard, E.J.
 TITLE Human monocyte chemoattractant protein-1 (MCP-1)
 JOURNAL Adv. Exp. Med. Biol. 305, 47-56 (1991)
 MEDLINE 92095166
 PUBMED 1661560
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 71513] from the original journal article.
 This sequence comes from 2.
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"


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gene 1..739 /db_xref="taxon:9606"
CDS 54..353 /gene="monocyte chemoattractant protein-1, MCP-1"
/note="This sequence comes from 2, MCP-1"
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Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCCAGATGCAATCAATGCCCGCAGTCACTGCTGTATTAACCTCACCATAAGAGATC 60
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Db 183 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACAGCAGCAAGTGTCCCAAGAAGCT 242
Qy 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 180
Db 243 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 302
Qy 181 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 228
Db 303 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 350
RESULT 15
Al7786 741 bp mRNA linear PAT 30-SEP-1994
LOCUS MCP-1 mRNA.
DEFINITION MCP-1 mRNA.
ACCESSION Al7786
VERSION Al7786.1 GI:641144
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 741)
AUTHORS Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.
TITLE Protein with cytokine activity, recombinant DNA, expression vector
and hosts for obtaining it
JOURNAL Patent: EP 0488900-A 25 03-JUN-1992;
ELF SANOFI
FEATURES
source
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/organism="unidentified"
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70..369
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/db_xref="GI:641143"
/db_xref="SWISS-PROT:P13500"
/translation="MKVSAALLCLLLIAATFIPQGLAOPDAINAPVTCYVNFNRRKIS
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ORIGIN
Query Match 100.0%; Score 228; DB 6; Length 741;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCCAGATGCAATCAATGCCCGCAGTCACTGCTGTATTAACCTCACCATAAGAGATC 60
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Db 139 CAGCCAGATGCAATCAATGCCCGCAGTCACTGCTGTATTAACCTCACCATAAGAGATC 198
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Qy 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 180
Db 259 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAAGTGGGTT 318
Qy 181 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 228
Db 319 CAGGATTCATGGACCACTGGACAAGCAACCCAACTCCGAAGACT 366
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Search completed: August 31, 2004, 03:22:47
Job time : 1394 secs

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PT neutralization antibody.
 XX Disclosure, Page 32; 39pp; Japanese.
 XX The invention relates to preventives and remedies for pulmonary hypertension, comprising an antagonistic inhibitory mutant of monocyte chemoattractant protein-1 (MCP-1). DNA encoding the mutant MCP-1, or a neutralising antibody against MCP-1. MCP-1 is a member of the C-C chemokine family. The preventives and remedies have hypotensive activity and can be used in the prevention and treatment of pulmonary hypertension particularly pulmonary primary hypertension. The present sequence represents DNA encoding wild-type human MCP-1
 XX Sequence 228 BP; 71 A; 62 C; 53 G; 42 T; 0 U; 0 Other;
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Query Match 100.0%; Score 228; DB 6; Length 228;
 Best Local Similarity 100.0%; Pred. No. 3.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACTTACCAATAGGAAGATC 60
 DB 1 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACTTACCAATAGGAAGATC 60

QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAAGTGTCCAAAGAAGCT 120
 DB 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAAGTGTCCAAAGAAGCT 120

QY 121 GTGATCTTCAAGACCATTTGSCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 121 GTGATCTTCAAGACCATTTGSCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180

QY 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228
 DB 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228

RESULT 2
 ID ABL60575 standard; DNA; 300 BP.
 XX ABL60575;
 AC ABL60575;
 XX 27-AUG-2002 (first entry)
 DT Human monocyte chemoattractant protein-1 (MCP-1) related DNA.
 DE MCP-1; hepatic disease; monocyte chemoattractant protein-1; liver;
 KW fibrosis; cirrhosis; hepatotropic; human; ds.
 XX Homo sapiens.
 OS WO200230464-A1.
 PN 18-APR-2002.
 XX 28-SEP-2001; 2001WO-JP008552.
 PF 11-OCT-2000; 2000JP-00310604.
 PR (DAUC) DAIICHI PHARM CO LTD.
 XX (EGAS/) EGASHIRA K.
 PI Egashira K, Takeshita A, Koyanagi M, Nakamura M, Nishida K;
 DR WPI; 2002-394437/42.
 XX Agents for treating hepatic diseases comprise a monocyte chemoattractant protein-1 function inhibitor.
 PS Disclosure, Page 10; 18pp; Japanese.
 XX The invention provides agents for treating and preventing hepatic diseases. The agents contain a monocyte chemoattractant protein-1 (MCP-1)

CC function inhibitor as the active ingredient. The MCP-1 function inhibitors are useful in treating and preventing hepatic diseases such as liver fibrosis or liver cirrhosis. The present sequence represents a human MCP-1 related DNA sequence
 XX Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 228; DB 6; Length 300;
 Best Local Similarity 100.0%; Pred. No. 3.8e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACTTACCAATAGGAAGATC 60
 DB 70 CAGCCAGATGCAATCAATGCCCCCAGTCACTGCTGTATATACTTACCAATAGGAAGATC 129

QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAAGTGTCCAAAGAAGCT 120
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QY 121 GTGATCTTCAAGACCATTTGSCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 190 GTGATCTTCAAGACCATTTGSCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 249

QY 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 228
 DB 250 CAGGATTCATGGACCACTGGACAAAGCAAAACCCAACTCCGAAGACT 297

RESULT 3
 ID ACC42732 standard; DNA; 300 BP.
 XX ACC42732;
 AC ACC42732;
 XX 06-AUG-2003 (first entry)
 DT Monocyte chemotactic protein 1, MCP-1, related sequence, SEQ ID 1.
 DE Human; immunosuppressive; organ transplant rejection; arteriosclerosis; endothelial thickening; monocyte chemotactic protein 1; MCP-1; ds.
 XX Homo sapiens.
 OS WO2003037376-A1.
 PN 08-MAY-2003.
 XX 01-NOV-2002; 2002WO-JP011441.
 PF 02-NOV-2001; 2001JP-00337861.
 PR (EGAS/) EGASHIRA K.
 XX Egashira K, Takeshita A, Sata M;
 PI WPI; 2003-457365/43.
 DR Prevention or treatment of organ transplant rejection, comprises using monocyte chemotactic protein 1 to inhibit endothelial thickening or arteriosclerosis of homograft or allograft blood vessels.
 XX Claim 6; Page 13; 20pp; Japanese.
 PS The present invention relates to a method for preventing or treating organ transplant rejection. The method comprises preventing arteriosclerosis or endothelial thickening in blood vessel autograft or CC allograft, post-transplant, using an agent which inhibits the function of monocyte chemotactic protein 1 (MCP-1). The present sequence was used to illustrate the method of the invention
 XX Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 228; DB 7; Length 300;

Best Local Similarity 100.0%; Pred. No. 3.8e-62;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTCACCATAAGAGATC 60
DB 70 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTCACCATAAGAGATC 129
QY 61 TCAGTCGAGAGGCTCGGAGCTATAGAAATATCAGCAGCAGAGTGTCCCAAGAGCT 120
DB 130 TCAGTCGAGAGGCTCGGAGCTATAGAAATATCAGCAGCAGAGTGTCCCAAGAGCT 189
QY 121 GTGATCTTCAGACCATGTCGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 190 GTGATCTTCAGACCATGTCGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 249
QY 181 CAGGATTCATGAGCACCCTGGACCAAGCAACCAACCACTCGAGACT 228
DB 250 CAGGATTCATGAGCACCCTGGACCAAGCAACCAACCACTCGAGACT 297

RESULT 4
ABV97697/C
ID ABV97697 standard; cDNA; 475 BP.
AC ABV97697;
XX
XX 14-JAN-2003 (first entry)
DE Human pancreatic cancer expressed cDNA SEQ ID NO 3105.
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW Cystostatic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200260317-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 30-JAN-2002; 2002WO-US002781.
EF
XX
XX 30-JAN-2001; 2001US-0265305P.
PR
XX 31-JAN-2001; 2001US-0265682P.
PR
XX 09-FEB-2001; 2001US-0267568P.
PR
XX 21-MAR-2001; 2001US-0278651P.
PR
XX 28-APR-2001; 2001US-0287112P.
PR
XX 16-MAY-2001; 2001US-0291631P.
PR
XX 12-JUL-2001; 2001US-0305484P.
PR
XX 20-AUG-2001; 2001US-0313999P.
PR
XX 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI
XX
XX WPI; 2002-627435/67.
DR
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX Claim 1; SEQ ID NO 3105; 300pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC

CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at fip.wipo.int/pub/published_pct_sequences
XX
XX Sequence 475 BP; 134 A; 90 C; 122 G; 129 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 228; DB 6; Length 475;
Best Local Similarity 100.0%; Pred. No. 4.6e-62;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTCACCATAAGAGATC 60
DB 404 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTCACCATAAGAGATC 345
QY 61 TCAGTCGAGAGGCTCGGAGCTATAGAAATATCAGCAGCAGAGTGTCCCAAGAGCT 120
DB 344 TCAGTCGAGAGGCTCGGAGCTATAGAAATATCAGCAGCAGAGTGTCCCAAGAGCT 285
QY 121 GTGATCTTCAGACCATGTCGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 284 GTGATCTTCAGACCATGTCGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 225
QY 181 CAGGATTCATGAGCACCCTGGACCAAGCAACCAACCACTCGAGACT 228
DB 224 CAGGATTCATGAGCACCCTGGACCAAGCAACCAACCACTCGAGACT 177

RESULT 5
ABS68800
ID ABS68800 standard; RNA; 647 BP.
XX
XX ABS68800;
AC
XX
XX 20-NOV-2002 (first entry)
DT
XX
XX Human monocyte chemoattractant protein-1 (hMCP-1) RNA.
DE
XX
XX Phosphoramidite; INVADER assay cleavage reaction; FEN1; cleavage;
KW nucleic acid separation; DNA polymerase; human; MCP-1; ubiquitin;
KW monocyte chemoattractant protein-1; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200263030-A2.
PN
XX
XX 15-AUG-2002.
PD
XX
XX 06-FEB-2002; 2002WO-US003423.
PF
XX
XX 06-FEB-2001; 2001US-00777430.
PR
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX
XX Lyamichiev V, Skrzypczynski Z, Allawi HT, Wayland SR, Takova T;
PI Neri BP;
PI
XX
XX WPI; 2002-674850/72.
DR
XX
XX Composition useful for e.g. separation of nucleic acids comprises a
PT positively or neutrally charged phosphoramidite.
PT
XX
XX Example 14; Page 194; 197pp; English.
PS
XX
XX The invention relates to a composition comprising a positively or
CC neutrally charged phosphoramidite. The composition is useful for
CC separation of nucleic acid molecules. The composition is further useful
CC for fractionation of specific nucleic acids by selective charge reversal
CC in e.g. INVADER assay cleavage reactions; and in the synthesis of
CC charge-balanced molecules. In the fractionation of nucleic acid
CC

CC molecules, the method provides an absolute readout of the partition of
 CC products from substrates (i.e. provides a 100% separation). Through the
 CC use of multiple positively charged adducts, synthetic molecules can be
 CC constructed with sufficient modification due to the fact that the
 CC normally negatively charged strand is made nearly neutral. It is also
 CC possible to distinguish between a enzymatically or thermally degraded DNA
 CC fragments due to the absence or presence of 3'phosphate. ABS68740-
 CC ABS68813 represent coding sequences and primers used in the method of the
 CC invention
 XX
 SQ Sequence 647 BP; 180 A; 146 C; 121 G; 0 T; 200 U; 0 Other;

Query Match 100.0%; Score 228; DB 6; Length 647;
 Best Local Similarity 81.6%; Pred. No. 5.2e-62;
 Matches 186; Conservative 42; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGACCTGCTGTTTATTAACCTTCAACCAATAGGAATC 60
 DB 70 CAGCCAGATGCAATCAATGCCCGACCTGCTGTTTATTAACCTTCAACCAATAGGAATC 129
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAAGATATCAGCAGCAAGTGTCCCAAGAAGCT 120
 DB 130 UCAGUGCAGAGCTCGCGAGCTATAGAAGATATCAGCAGCAAGTGTCCCAAGAAGCT 189
 QY 121 GTGATCTTCAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 190 GUGAUCUUCAGACCAUUGUGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 249
 QY 181 CAGGATTCATGACCACTGCGACCAAGCAAAACCCAACTCCGAAGACT 228
 DB 250 CAGGAUCCAGGACCACTGCGACCAAGCAAAACCCAACTCCGAAGACT 297

RESULT 6
 AAQ85370
 ID AAQ85370 standard; cDNA; 725 BP.
 XX
 AC AAQ85370;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-AUG-1995 (first entry)
 XX
 DE Chemoattractant protein MCP-1.
 XX
 KW MCP-1; chemoattractant; heparanase; heparin; heparan sulfate; arthritis;
 KW restenosis; cancer; wound healing; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9504158-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 26-JUL-1994; 94WO-US008207.
 XX
 PR 29-JUL-1993; 93US-00099866.
 PR 13-OCT-1993; 93US-00136117.
 XX
 PA (UPJO) UPJOHN CO.
 XX
 PI Hoogwerf AJ, Ledbetter SR;
 XX
 DR WPI; 1995-082239/11.
 DR P-PSDB; AAR70800.
 XX
 PT Screening for cpds. with anti-heparanase activity - by detecting
 PT inhibition of heparin or heparan sulphate degradation, potentially useful
 PT for treating arthritis, restenosis, cancer.
 XX
 PS Disclosure; Page 49-50; 60pp; English.
 CC Purified heparanases, prepared under reducing conditions and activated
 CC with transglutaminase, are given in AAR70786-805. Most are prepared by

CC reverse transcription of mRNA from activated human leukocytes, then
 CC cloning of the cDNA into pVL1392 baculovirus vector, and expression in
 CC Sf9 cells in the presence of reduced glutathione and dithiothreitol.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 2; Length 725;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGACCTGCTGTTTATTAACCTTCAACCAATAGGAATC 60
 DB 123 CAGCCAGATGCAATCAATGCCCGACCTGCTGTTTATTAACCTTCAACCAATAGGAATC 182
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAAGATATCAGCAGCAAGTGTCCCAAGAAGCT 120
 DB 183 TCAGTGCAGAGCTCGCGAGCTATAGAAGATATCAGCAGCAAGTGTCCCAAGAAGCT 242
 QY 121 GTGATCTTCAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 243 GTGATCTTCAGACCATTTGCGCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 302
 QY 181 CAGGATTCATGACCACTGCGACCAAGCAAAACCCAACTCCGAAGACT 228
 DB 303 CAGGATTCATGACCACTGCGACCAAGCAAAACCCAACTCCGAAGACT 350

RESULT 7
 AAX80631
 ID AAX80631 standard; cDNA; 725 BP.
 XX
 AC AAX80631;
 XX
 DT 29-SEP-1999 (first entry)
 XX
 DE Monocyte chemoattractant protein-1 gene.
 XX
 KW Monocyte chemoattractant protein-1; MCP-1; chemokine; vaccine; antigen;
 KW immune response; DNA vaccine; humoral response; cell-mediated response;
 KW PCR; gene regulatory element; expression plasmid vector; ss.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH CDS 54..353
 FT /*tag= a
 FT /product= "Monocyte chemoattractant preprotein"
 FT sig_peptide 54..122
 FT /*tag= b
 FT mat_peptide 123..350
 FT /*tag= c
 FT /label= Monocyte chemoattractant protein_1
 FT /function= "Chemotactic for monocytes"
 FT misc_feature 707..712
 FT /*tag= e
 FT /note= "potential polyA signal"
 FT polyA_site 725
 FT /*tag= f

WO9929728-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 11-DEC-1998; 98WO-US026291.
 XX
 PR 11-DEC-1997; 97US-0069281P.
 XX
 PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX
 PI Gallo RC, Devico AL, Garzino-Demo A;
 XX
 DR WPI; 1999-385578/32.

DR WPI; 2003-278396/27.
 XX Characterizing prostate tissue comprises providing a prostate tissue
 PT sample from a subject and detecting the presence or absence of expression
 PT of hepsin, pim-1 or E2H2.
 XX
 PS Disclosure; SEQ ID NO 66; 297pp; English.
 XX
 XX This invention relates to a novel method of characterizing prostate
 CC tissue in a subject and to compositions and methods for cancer
 CC diagnostics, including cancer markers, in particular prostate cancer.
 CC Prostate cancer (PCA) is a leading cause of male cancer-related death.
 CC Additional serum and tissue biomarkers would aid diagnosis. The invention
 CC may provide means of producing compounds with a cytostatic activity or
 CC allow the development of gene therapy. The methods of the invention
 CC useful for characterizing prostate tissue in a subject, screening
 CC compounds, characterizing inconclusive prostate biopsy tissue in a
 CC subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase)
 CC expression in a bodily fluid, characterizing tissue in a subject,
 CC diagnosing cancer in a subject and inhibiting the growth of cells. The
 CC present sequence is a DNA sequence which is preferably utilised in the
 CC method of the invention.
 XX
 SQ Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;

Query Match 100.0%; Score 228; DB 9; Length 725;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCAGAGAGATC 60
 Db 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCAGAGAGATC 182
 QY 61 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAAGTGTCCCAAGAGCT 120
 Db 183 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAAGTGTCCCAAGAGCT 242
 QY 121 GTGATCTTCAAGACCATTTGCGCCAGGAGATCTGTGCTGACCCCAAGAGTGGTT 180
 Db 243 GTGATCTTCAAGACCATTTGCGCCAGGAGATCTGTGCTGACCCCAAGAGTGGTT 302
 QY 181 CAGGATTCATGACCACTGCGAGCAAGCAAAACCCAACTCCGAAGACT 228
 Db 303 CAGGATTCATGACCACTGCGAGCAAGCAAAACCCAACTCCGAAGACT 350

RESULT 10
 ADE84839
 ID ADE84839 standard; DNA; 725 BP.
 AC ADE84839;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #58.
 XX ss; cytostatic; farnesyl transferase inhibitor; gene expression;
 KW quinalinone; leukemia; cancer.
 XX
 XX Homo sapiens.
 OS
 PN WO2003038129-A2.
 XX
 XX 08-MAY-2003.
 PD
 XX 30-OCT-2002; 2002WO-US034784.
 PF
 XX 30-OCT-2001; 2001US-0338997P.
 PR 30-OCT-2001; 2001US-0340081P.
 PR 30-OCT-2001; 2001US-0340938P.
 PR 30-OCT-2001; 2001US-0341012P.
 XX
 XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX Raponi M;
 XX WPI; 2003-513497/48.
 DR
 XX
 PT Determining whether a patient will respond to treatment with a farnesyl
 PT transferase inhibitor, by analyzing the expression of gene that is
 PT differentially modulated in the presence of the inhibitor.
 XX
 PS Disclosure; SEQ ID NO 58; 346pp; English.
 XX
 XX The invention relates to a method of determining whether a patient will
 CC respond to treatment with a farnesyl transferase inhibitor (FTI) by
 CC analyzing the expression of gene that is differentially modulated in the
 CC presence of an FTI. The method is useful for determining whether a
 CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
 CC chlorophenyl)]-1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
 CC methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
 CC patient with leukemia with FTI if the analysis indicates that the patient
 CC will respond. This sequence corresponds to a gene whose expression may be
 CC modulated in the presence of FTI.
 XX

SQ Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 9; Length 725;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCAGAGAGATC 60
 Db 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCAGAGAGATC 182
 QY 61 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAAGTGTCCCAAGAGCT 120
 Db 183 TCAGTCAGAGGCTCGCGAGCTATAGAGATCAACAGCAAGTGTCCCAAGAGCT 242
 QY 121 GTGATCTTCAAGACCATTTGCGCCAGGAGATCTGTGCTGACCCCAAGAGTGGTT 180
 Db 243 GTGATCTTCAAGACCATTTGCGCCAGGAGATCTGTGCTGACCCCAAGAGTGGTT 302
 QY 181 CAGGATTCATGACCACTGCGAGCAAGCAAAACCCAACTCCGAAGACT 228
 Db 303 CAGGATTCATGACCACTGCGAGCAAGCAAAACCCAACTCCGAAGACT 350

RESULT 11
 AAN91337
 ID AAN91337 standard; cDNA; 738 BP.
 XX
 AC AAN91337;
 XX
 XX 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 25-JUL-1989 (first entry)
 XX
 XX DNA which encodes human monocyte chemo-attractant peptide-1.
 DE Human monocyte chemo-attractant peptide; inflammatory disease; neoplasms;
 XX ss.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 53..350
 FT /tag= a
 FT mat_peptide 120..347
 FT /tag= c
 FT polyA_signal /label= mature MCP-1
 FT 705..709
 FT /tag= b
 XX
 PN USN7330446-N.

KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
 KW preeclampsia; atherosclerosis; inflammatory condition; wound healing;
 KW inflammation; erythropoiesis; hair loss; human; gene; ds.
 OS Homo sapiens.
 XX WO200246465-A2.
 PN 13-JUN-2002.
 XX 10-DEC-2001; 2001WO-GB005458.
 XX 08-DEC-2000; 2000GB-00030076.
 PR 08-FEB-2001; 2001GB-00003156.
 PR 25-OCT-2001; 2001GB-00025666.
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
 PI Rayner WN;
 XX WPI; 2002-627238/67.
 DR Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT types under different conditions and identifying a differentially
 PT regulated gene.

XX Claim 37; Page 399; 538pp; English.

XX The present invention relates to methods for identifying genes and
 CC proteins that are implicated in a specific disease or physiological
 CC condition. The method comprises comparing the transcriptome/proteome of a
 CC specialised cell type implicated in a disease or condition with that of a
 CC second specialised cell type, under two experimental conditions, and
 CC identifying a gene that is differentially regulated in the two
 CC specialised cell types under experimental conditions. ABV7873-ABV78116
 CC and ABP65061-ABP65257 were identified using the methods of the invention.
 CC The coding sequences and proteins are useful for treating a disease in a
 CC patient, for manufacture of a medicament for treating hypoxia-regulated
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
 CC biological response to hypoxia conditions, or hypoxic-associated
 CC pathology in a patient. The coding sequences and proteins are also useful
 CC for monitoring the therapeutic treatment of a disease or physiological
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,
 CC retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss

XX SQ Sequence 739 BP; 222 A; 171 C; 126 G; 220 T; 0 U; 0 Other;

Query Match 100.0%; Score 228; DB 6; Length 739;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTTCAACCAATAGGAAGATC 60
 DB 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTTCAACCAATAGGAAGATC 182
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGATCAACAGCAATCAACAGCAAGTGTCCCAAGAGACT 120
 DB 183 TCAGTGCAGAGCTCGCGAGCTATAGAGATCAACAGCAATCAACAGCAAGTGTCCCAAGAGACT 242
 QY 121 GTGATCTTCAAGACCATTTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT 180
 DB 243 GTGATCTTCAAGACCATTTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT 302
 QY 181 CAGGATTCATGGACCTGGACAGCAACCAACCACTCCGAAGACT 228
 DB 303 CAGGATTCATGGACCTGGACAGCAACCAACCACTCCGAAGACT 350

RESULT 14
 ABZ34738

ID ABZ34738 standard; cDNA; 739 BP.
 XX ABZ34738;
 AC 04-FEB-2003 (first entry)
 DT Coding sequence SEQ ID 96, downregulated in osteogenesis.
 XX Osteopathic; osteogenesis modulator; gene therapy; osteogenesis;
 KW osteoporosis; bone disease; downregulator; human; ss.
 XX Homo sapiens.
 OS WO200281745-A2.
 PN 17-OCT-2002.
 XX 05-APR-2002; 2002WO-IB002211.
 PF 05-APR-2001; 2001US-0281400P.
 PR (AVET) AVENTIS PHARMA SA.
 XX Garcia T, Roman Roman S, Baron R, Call K, Theilhaber J;
 PI Connolly T, Jackson A, Bushnell SE, Rawadi G;
 XX WPI; 2003-058567/05.
 DR Novel isolated nucleic acid upregulated/downregulated in osteogenesis,
 PT useful for bone disease therapy in subject.
 PT Claim 27; Page 124-125; 237pp; English.
 XX The present invention relates to novel nucleotide sequences, which are
 CC differentially expressed in models of osteogenesis upon being put in
 CC contact with a stimulator of osteogenesis. The present sequence is one
 CC such sequence. This sequence can be used for diagnosing osteoporosis/bone
 CC disease in a patient, promoting osteogenesis and/or preventing
 CC osteoporosis/bone disease. The present sequence encodes a secreted
 CC protein

XX SQ Sequence 739 BP; 222 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 7; Length 739;
 Best Local Similarity 100.0%; Pred. No. 5.4e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTTCAACCAATAGGAAGATC 60
 DB 123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTTCAACCAATAGGAAGATC 182
 QY 61 TCAGTGCAGAGCTCGCGAGCTATAGAGATCAACAGCAATCAACAGCAAGTGTCCCAAGAGACT 120
 DB 183 TCAGTGCAGAGCTCGCGAGCTATAGAGATCAACAGCAATCAACAGCAAGTGTCCCAAGAGACT 242
 QY 121 GTGATCTTCAAGACCATTTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT 180
 DB 243 GTGATCTTCAAGACCATTTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT 302
 QY 181 CAGGATTCATGGACCTGGACAGCAACCAACCACTCCGAAGACT 228
 DB 303 CAGGATTCATGGACCTGGACAGCAACCAACCACTCCGAAGACT 350

RESULT 15

AAA34899
 ID AAA34899 standard; DNA; 741 BP.
 XX AAA34899;
 XX 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2588.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 XX PD 24-FEB-2000.
 XX
 XX PF 03-AUG-1999; 99WO-US017712.
 XX
 XX PR 03-AUG-1998; 98US-0095212P.
 XX
 XX PA (UYEC-) UNIV EAST CAROLINA.
 XX
 XX PI Nyce JW;
 XX
 XX DR WPI; 2000-205971/18.
 XX
 XX PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX PS Disclosure; Page 761-762; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (CN) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 XX Sequence 741 BP; 214 A; 173 C; 133 G; 221 T; 0 U; 0 Other;
 Query Match 100.0%; Score 228; DB 3; Length 741;
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTTTACTTCCACCAATAGGAGATC 60
 DB 139 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTTTAACTTCCACCAATAGGAGATC 198
 QY 61 TCAGTGCAGAGGCTCGCAGGCTATAGAGAAATCAGCAGCAAGTGTCCCAAGAGAGCT 120
 DB 199 TCAGTGCAGAGGCTCGCAGGCTATAGAGAAATCAGCAGCAAGTGTCCCAAGAGAGCT 258

QY 121 GTGATCTTCAAGACCACTTGTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
 DB 259 GTGATCTTCAAGACCACTTGTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 318
 QY 181 CAGGATTCATGGAGACCACTGTGACCAAGCAAAACCCAACTCCGAGAGACT 228
 DB 319 CAGGATTCATGGAGACCACTGTGACCAAGCAAAACCCAACTCCGAGAGACT 366

Search completed: August 31, 2004, 02:58:29
 Job time : 241 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:11 ; Search time 54 Seconds

(without alignments)
2343.126 Million cell updates/sec

Title: 07330446

Perfect score: 228

Sequence: 1 cagccagatgcaatcaatgc.....aaacccaactccgaagact 228

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	228	100.0	725	4	US-09-591-992-3
2	228	100.0	725	4	US-09-023-655-1344
3	228	100.0	741	3	US-07-927-391-25
4	228	100.0	741	4	US-09-023-655-1165
5	227.6	99.8	1712	4	US-09-148-545-106
6	227.6	99.8	1822	4	US-09-148-545-105
7	226.4	99.3	231	5	PCT-US95-00605-2
8	224.8	98.6	228	1	US-08-250-958-3
9	217.4	95.4	752	6	5212073-1
10	196	85.0	213	4	US-09-463-451-29
11	196	85.0	213	4	US-09-463-451-30
12	148.2	65.0	228	3	US-07-927-391-13
13	148.2	65.0	810	4	US-09-016-434-1273
14	148.2	65.0	814	3	US-07-927-391-15
15	147.2	64.6	247	3	US-07-927-391-17
16	139.6	61.2	294	4	US-09-023-655-901
17	139.6	61.2	605	4	US-09-366-887A-26
18	139.6	61.2	807	4	US-09-023-655-978
19	139	61.0	840	4	US-09-016-434-1033
20	138	60.5	813	4	US-09-016-434-1156
21	135.4	59.4	207	4	US-09-463-458A-28
22	135	59.2	315	3	US-08-744-419-3
23	135	59.2	514	4	US-09-545-894-3
24	135	59.2	540	3	US-08-744-419-1
25	134.4	58.9	207	4	US-09-463-458A-8
26	134.4	58.9	207	4	US-09-463-458A-25
27	127.2	55.8	400	4	US-09-833-381-1234

28	125.6	55.1	297	3	US-08-613-822-3	Sequence 3, Appli
29	125.6	55.1	297	3	US-08-852-212-1	Sequence 1, Appli
30	125.6	55.1	297	4	US-09-479-729B-3	Sequence 3, Appli
31	125.6	55.1	297	4	US-09-261-201A-3	Sequence 3, Appli
32	125.6	55.1	297	4	US-09-717-209-3	Sequence 3, Appli
33	125.6	55.1	802	4	US-09-016-434-687	Sequence 687, App
34	125.6	55.1	823	4	US-09-545-894-1	Sequence 1, Appli
35	111	48.7	818	4	US-09-366-887A-15	Sequence 15, Appli
36	109.6	48.1	994	4	US-09-366-887A-5	Sequence 5, Appli
37	99.2	43.5	1047	4	US-09-546-028-44	Sequence 44, Appli
38	99.2	43.5	1080	4	US-09-546-028-39	Sequence 39, Appli
39	99.2	43.5	1086	4	US-09-546-028-37	Sequence 37, Appli
40	99.2	43.5	1113	4	US-09-546-028-38	Sequence 38, Appli
41	99.2	43.5	1805	4	US-09-646-028-45	Sequence 45, Appli
42	95.2	41.8	121	4	US-09-463-458A-4	Sequence 4, Appli
43	88	38.6	272	4	US-09-023-655-845	Sequence 845, App
44	86.8	38.1	253	4	US-09-833-381-1229	Sequence 1229, Ap
45	72	31.6	353	4	US-09-366-887A-21	Sequence 21, Appli

ALIGNMENTS

RESULT 1

US-09-591-992-3

; Sequence 3, Application US/09591992

; Patent No. 6569418

; GENERAL INFORMATION:

; APPLICANT: Gallo, Robert C.

; APPLICANT: Garzino, Alfredo

; TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination

; FILE REFERENCE: 4115-109 CIP

; CURRENT APPLICATION NUMBER: US/09/591,992

; CURRENT FILING DATE: 2000-06-12

; PRIOR APPLICATION NUMBER: PCT/US98/26291

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/186,416

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/069,281

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 725

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-591-992-3

Query Match 100.0%; Score 228; DB 4; Length 725;
Best Local Similarity 100.0%; Pred.No. 3.8e-61; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0;

Qy	1	CAGCCAGATGCAATCAATGCCCGAGTCACTGTGTATTAATTCACCAATAGGAATC	60
Db	123	CAGCCAGATGCAATCAATGCCCGAGTCACTGTGTATTAATTCACCAATAGGAATC	182
Qy	61	TCAGTCGAGAGGTCGCGAGCTATAGAGATCACCAGAGCAAGTGTCCCAAGAGCT	120
Db	183	TCAGTCGAGAGGTCGCGAGCTATAGAGATCACCAGAGCAAGTGTCCCAAGAGCT	242
Qy	121	GTGATCTTCAAGACCAATTGTGGCCCAAGGAGATGTGTGCTGACCCCAAGCAAGTGGTT	180
Db	243	GTGATCTTCAAGACCAATTGTGGCCCAAGGAGATGTGTGCTGACCCCAAGCAAGTGGTT	302
Qy	181	CAGATTCCATGGACCACTGGACAGCAAAACCCAACTCCGAAGACT	228
Db	303	CAGATTCCATGGACCACTGGACAGCAAAACCCAACTCCGAAGACT	350

RESULT 2

US-09-023-655-1344

; Sequence 1344, Application US/09023655

NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/POCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0855
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: G187434
US-09-023-655-1165

Query Match 100.0%; Score 228; DB 4; Length 741;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGATGCAATCAATGCCAGTCCAGTCTGTATTAATCTTCAACAATAGGAATC 60
DB 139 CAGCAGATGCAATCAATGCCAGTCCAGTCTGTATTAATCTTCAACAATAGGAATC 198

QY 61 TCAGTGCAGAGGCTCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 199 TCAGTGCAGAGGCTCGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 258

QY 121 GTGATCTTCAAGACCATTTGTGCGCAAGAGAGATCTGTCTGACCCCAAGCAGAGTGGGTT 180
DB 259 GTGATCTTCAAGACCATTTGTGCGCAAGAGAGATCTGTCTGACCCCAAGCAGAGTGGGTT 318

QY 181 CAGATTCTCAGACCATCTGACAGCAAGCAAACTCCGAAGACT 228
DB 319 CAGATTCTCAGACCATCTGACAGCAAGCAAACTCCGAAGACT 366

RESULT 5
US-09-148-545-106
Sequence 106, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162

EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
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EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
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EARLIER APPLICATION NUMBER: 60/047,597
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
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EARLIER APPLICATION NUMBER: 60/048,974
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EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
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EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,892
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EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
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EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
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EARLIER APPLICATION NUMBER: 60/056,909
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 106
LENGTH: 1712

Query Match 99.8%; Score 227.6; DB 4; Length 1712;
Best Local Similarity 99.6%; Pred. No. 6.9e-61;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCACTGCTGTATTAATCCCAATAGGAAGATC 60
Db 1059 CAGCCAGATGCAATCAATGCCCCAGTCCACTGCTGTATTAATCCCAATAGGAAGATC 1118
QY 61 TCAGTCAGAGGCTCCGAGCTATAGAGATCAGCAGCAGCAAGTGTCCCAAGAGCT 120
Db 1119 TCAGTCAGAGGCTCCGAGCTATAGAGATCAGCAGCAGCAAGTGTCCCAAGAGCT 1178
QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAGCAAGTGTGGTT 180
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QY 181 CAGGATTCATGAGCACCCTGGACAGCAAAACCAAACTCCGAAGACT 228
Db 1239 CAGGATTCATGAGCACCCTGGACAGCAAAACCAAACTCCGAAGACT 1286

RESULT 6
US-09-148-545-105
; Sequence 105, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1

EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
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EARLIER APPLICATION NUMBER: 60/056,632
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EARLIER APPLICATION NUMBER: 60/056,664
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EARLIER APPLICATION NUMBER: 60/056,876
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EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
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EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
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EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 1822

Query Match 99.8%; Score 227.6; DB 4; Length 1822;
Best Local Similarity 99.6%; Pred. No. 7e-61;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTTTAACTTCAACCAATAGGAATC 60
DB 1169 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTTTAACTTCAACCAATAGGAATC 1228
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAAATACACGAGCAAGTGTCCCAAGAAGCT 120
DB 1229 TCAGTGCAGAGGCTCGGAGCTATAGAGAAATACACGAGCAAGTGTCCCAAGAAGCT 1288
QY 121 GTGATCTTCAAGACATTTGGCCCAAGAGATCTGTGCTGACCCCAAGCAAGTGTGGTT 180
DB 1289 GTGATCTTCAAGACATTTGGCCCAAGAGATCTGTGCTGACCCCAAGCAAGTGTGGTT 1348
QY 181 CAGGATTCATGGACCACTGGACAAACCAACCAAACTCCGAAGCT 228
DB 1349 CAGGATTCATGGACCACTGGACAAACCAACCAAACTCCGAAGCT 1396

RESULT 7
US-095-00605-2
; Sequence 2, Application PC/TUS9500605

GENERAL INFORMATION:
APPLICANT: Lyle, Leon
APPLICANT: Thomas-Miller, Beth
TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: VASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mallinckrodt Medical, Inc.
STREET: 675 McDonnell Boulevard, P.O. Box 5840
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00605
FILING DATE: 13-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,917
FILING DATE: 14-JAN-1994
APPLICATION NUMBER: US 07/965,678
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vacca, Rita D.
REGISTRATION NUMBER: 33,624
REFERENCE/DOCKET NUMBER: 0783.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-895-7215
TELEFAX: 314-895-2156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Monocyte Chemotactic Protein-1
STRAIN: human
PCT-US95-00605-2

Query Match 99.3%; Score 226.4; DB 5; Length 231;
Best Local Similarity 81.1%; Pred. No. 7.7e-61;
Matches 185; Conservative 42; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTTTAACTTCAACCAATAGGAATC 60
DB 4 CAGCCAGATGCAATCAATGCCCGCCAGTCACCTGCTGTTTAACTTCAACCAATAGGAATC 63
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAAATACACGAGCAAGTGTCCCAAGAAGCT 120
DB 64 UCAGUGCAGAGGCTCGGAGCTATAGAGAAATACACGAGCAAGTGTCCCAAGAAGCT 123
QY 121 GTGATCTTCAAGACATTTGGCCCAAGAGATCTGTGCTGACCCCAAGCAAGTGTGGTT 180
DB 124 GUGAUUUCAGACCAUUGUGCCCAAGAGAGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 183
QY 181 CAGGATTCATGGACCACTGGACAAACCAACCAAACTCCGAAGCT 228
DB 184 CAGGATTCATGGACCACTGGACAAACCAACCAAACTCCGAAGCT 231

RESULT 8
US-08-250-958-3
; Sequence 3, Application US/08250958
; Patent No. 5571713

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; GENERAL INFORMATION:
; APPLICANT: LYLE, LEON R.
; APPLICANT: KUNKEL, STEVEN L.
; APPLICANT: STRIETER, ROBERT M.
; TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
; TITLE OF INVENTION: VASCULAR RESTENOSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROHWELL, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,958
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,678
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 2077-206A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-250-958-3

Query Match 98.6%; Score 224.8; DB 1; Length 228;
Best Local Similarity 80.7%; Pred. No. 2.4e-60;
Matches 184; Conservative 42; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCCAGATGCATCAATCAATGCCCGCAGTCACCTGCTGTATTAACCTCACCACATAGGAAGATC 60
Db 1 CAGCCAGATGCATCAATCAATGCCCGCAGTCACCTGCTGTATTAACCTCACCACATAGGAAGATC 60
Qy 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAAGCT 120
Db 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAGAAAGCT 120
Qy 121 GTGATCTTCAAGACCATTTGTGCCAAGAGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Db 121 GTGATCTTCAAGACCATTTGTGCCAAGAGAGATCTGTGCTGACCCCAAGCAGAAAGTGGTT 180
Qy 181 CAGGATTCATGACCATCTGGACAGCAACCCAAACT 219
Db 181 CAGGATTCATGACCATCTGGACAGCAACCCAAACT 219
Qy 322 CAGGATTCATGACCATCTGGACAGCAACCCAAACT 360
Db 322 CAGGATTCATGACCATCTGGACAGCAACCCAAACT 360

RESULT 9
US-09-463-451-29
; Sequence 29, Application US/09463451
; Patent No. 6537779
; GENERAL INFORMATION:
; APPLICANT: KARA, Bupendra V.
; APPLICANT: PIOLI, David
; APPLICANT: BUNDELL, Kenneth R.
; APPLICANT: HOCKNEY, Robert C.
; TITLE OF INVENTION: T7 Promoter-Based Expression System
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/463,451
; FILING DATE: 03-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/02175
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: GB 9715660.8
; FILING DATE: 25-JUL-1997
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-463-451-29

Query Match 86.0%; Score 196; DB 4; Length 213;
Best Local Similarity 97.5%; Pred. No. 1.9e-51;
Matches 199; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 25 GTCACCTGCTGTATTAACCTCACCACATAGGAAGATCTCAGTCAGAGGCTCGGAGCTAT 84

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Db 4 GTTACTGCTGTTATTAATCTTACCAACCGTAAATCTCAGTGCAGAGGCTCGGAGCTAT 63
QY 85 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 144
Db 64 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 123
QY 145 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 204
Db 124 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 183
QY 205 AAGCAAAACCAAACTCCGAAGACT 228
Db 184 AAGCAAAACCAAACTCCGAAGACT 207

RESULT 11

US-09-463-451-30/c
; Sequence 30, Application US/09463451
; Patent No. 653779
; GENERAL INFORMATION:
; APPLICANT: KARA, Bupendra V.
; PIOLI, David
; BUNDELL, Kenneth R.
; HOCKNEY, Robert C.
; TITLE OF INVENTION: T7 Promoter-Based Expression System
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/463,451
; FILING DATE: 03-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/02175
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: GB 9715660.8
; FILING DATE: 25-JUL-1997

SEQUENCE CHARACTERISTICS:
; LENGTH: 213 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-463-451-30

Query Match 86.0%; Score 196; DB 4; Length 213;
Best Local Similarity 97.5%; Pred. No. 1.9e-51;
Matches 199; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 25 GTCACTGCTGTTATTAATCTTACCAATAGGAAGATCTCAGTGCAGAGGCTCGGAGCTAT 84
Db 210 GTTACTGCTGTTATTAATCTTACCAACCGTAAATCTCAGTGCAGAGGCTCGGAGCTAT 151
QY 85 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 144
Db 150 AGAAGATCACAGCAGCAGAGTGTCCAAAGAGCTGTGATCTTCAAGACCATTTGTGGCC 91
QY 145 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 204
Db 90 AAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTTTCAGGATTCATCGACACCATGGAC 31

QY 205 AAGCAAAACCAAACTCCGAAGACT 228
Db 30 AAGCAAAACCAAACTCCGAAGACT 7

RESULT 12

US-07-927-391-13
; Sequence 13, Application US/07927391
; Patent No. 6001649
; GENERAL INFORMATION:

; APPLICANT: CAFUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: MILOUX, Brigitte
; APPLICANT: MINTY, Adrian
; APPLICANT: VITA, Natalio

; TITLE OF INVENTION: Protein having a cytokin type
; TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA

; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/927,391
; FILING DATE: 19920929
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-07-927-391-13

Query Match 65.0%; Score 148.2; DB 3; Length 228;
Best Local Similarity 78.7%; Pred. No. 1.1e-36;
Matches 177; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGCAGCTACCTGCTGTTATTAATCTTCAAGACCATTTGTGGCC 60
Db 1 CAGCCAGATGCGGATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 60
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGACT 120
Db 61 CTTAAGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCGGAGACT 120
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGAGGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 121 GTAACTCTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
QY 181 CAGGATTCATCGACCTCGCAGCAGCAACCAACTCCGAG 225

RESULT 14

[illegible]

Qy

181 CAGGATTCCATGGACCACCTGGACAAGCAAACTCGAAG 225
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320 CAGGACTTATGAAGCACCTGGACAAGAAAACCCAATTCCAAAG 364

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Job time : 56 secs

RESULT 15
 US-07-927-391-17
 ; Sequence 17, Application US/07927391
 ; Patent No. 6001649
 ; GENERAL INFORMATION:
 ; APPLICANT: CAPUT, Daniel
 ; APPLICANT: FERRARA, Pascual
 ; APPLICANT: MILLOUX, Brigitte
 ; APPLICANT: MINTY, Adrian
 ; APPLICANT: VITA, Natalio
 ; TITLE OF INVENTION: Protein having a cytokin type
 ; TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
 ; TITLE OF INVENTION: for its preparation.
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: King Street Station, Suite 500, 1800 Diagonal
 ; STREET: Road, PO Box 299
 ; CITY: ALEXANDRIA
 ; STATE: VIRGINIA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/927,391
 ; FILING DATE: 19920929
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SAXE, Bernhard D
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 16781/369
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-9300
 ; TELEFAX: (703) 683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 247 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-07-927-391-17

Query Match 64.6%; Score 147.2; DB 3; Length 247;
Best Local Similarity 78.6%; Pred. No. 2.4e-36;
Matches 176; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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Qy		
16	CAGCGAGTTGGGATTAATTACTTCAACTACCTGCTGTACAGATTTTATCAATAGAAAAATC	75
Db		
61	TCAGTGTGACAGGCTCGCAGCTATAGAGAAATCACCAGCAGCAAGTGTCCCAAGAAGCT	120
Qy		
76	CCTAAGCAGAGGCTGGAGAGCTACAGAGGACACCCAGTAGCCACTGTCCCCGGGAAGCT	135
Db		
121	GTGATCTTCAAGACCAATTGTGGCCCAAGGAGATCTGTCTGACCCCAAGCAGAGAAGTGGGTT	180
Qy		
136	GTAACTTTCAGACCACCAACTGGACAGGAGATCTGTGCTGACCCACACAGAAAGTGGGTC	195
Db		
181	CAGGATTCATGGACACCTGGACAGCAAAACCCAAACTCCGAA	224
Qy		
196	CAGGACTTTATGAACACCTGGACAGAAAAACCCAAACTCCAAA	239
Db		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 02:59:34 ; Search time 254 Seconds

(without alignments)
4417.658 Million cell updates/sec

Title: 07330446

Perfect score: 228

Sequence: 1 cagccagatcaatcaatgc.....aaacccaactccgaagact 228

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	228	100.0	228	15	US-10-276-971-3
2	228	100.0	294	13	US-10-449-831A-209
3	228	100.0	405	13	US-10-449-831A-213
4	228	100.0	475	15	US-10-060-036-2105
5	228	100.0	647	9	US-09-777-430A-72
6	228	100.0	725	15	US-10-210-120-66
7	228	100.0	725	17	US-10-641-643-1344
8	228	100.0	725	17	US-10-283-975A-58
9	228	100.0	725	17	US-10-764-649-17
10	228	100.0	739	13	US-10-342-887-849
11	228	100.0	739	13	US-10-172-118-849
12	228	100.0	739	13	US-10-170-385-396
13	228	100.0	741	17	US-10-641-643-1165
14	228	100.0	756	15	US-10-133-013-210

15	228	100.0	757	13	US-10-388-360-377	Sequence 377, Appli
16	228	100.0	757	15	US-10-339-778-1	Sequence 1, Appli
17	228	100.0	783	15	US-10-133-013-209	Sequence 209, App
18	228	100.0	804	10	US-09-971-429B-18	Sequence 18, Appl
19	228	100.0	804	14	US-10-044-090-583	Sequence 583, App
20	228	100.0	978	9	US-09-792-793A-52	Sequence 52, Appl
21	228	100.0	978	16	US-10-375-209A-52	Sequence 52, Appl
22	228	100.0	984	9	US-09-792-793A-53	Sequence 53, Appl
23	228	100.0	984	16	US-10-375-209A-53	Sequence 53, Appl
24	228	100.0	999	9	US-09-792-793A-54	Sequence 54, Appl
25	228	100.0	999	16	US-10-375-209A-54	Sequence 54, Appl
26	228	100.0	1102	15	US-10-198-846-9822	Sequence 9822, Ap
27	227.6	99.8	1712	9	US-09-981-876-106	Sequence 106, App
28	227.6	99.8	1712	10	US-09-148-545-106	Sequence 106, App
29	227.6	99.8	1822	9	US-09-981-876-105	Sequence 105, App
30	227.6	99.8	1822	10	US-09-148-545-105	Sequence 105, App
31	226.4	99.3	473	15	US-10-060-036-2123	Sequence 2123, Ap
32	226.4	99.3	661	17	US-10-776-827-104	Sequence 104, App
33	226.4	99.3	685	8	US-08-927-939-76	Sequence 76, Appl
34	204	89.5	207	15	US-10-276-971-4	Sequence 4, Appli
35	202	88.6	276	13	US-10-424-599-120461	Sequence 120461,
36	193.2	84.7	338	14	US-10-040-739-793	Sequence 793, A
37	189.6	83.2	384	13	US-10-085-783A-52639	Sequence 52639, A
38	189.6	83.2	384	16	US-10-242-535A-52639	Sequence 52639, A
39	173	75.9	1005	15	US-10-133-013-211	Sequence 211, App
40	159.6	70.0	724	14	US-10-044-090-839	Sequence 839, App
41	148.2	65.0	810	13	US-10-170-385-464	Sequence 464, App
42	148.2	65.0	810	16	US-10-305-720-1273	Sequence 1273, Ap
43	148.2	65.0	817	14	US-10-044-090-837	Sequence 837, App
44	148.2	65.0	1085	8	US-08-927-939-81	Sequence 81, Appl
45	148.2	65.0	1085	17	US-10-717-597-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1

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US-10-276-971-3
; Sequence 3, Application US/10276971
; Publication No. US20030162737A1
; GENERAL INFORMATION:
; APPLICANT: Egashira Kensuke
; APPLICANT: Yoshikazu Yonemitsu
; APPLICANT: Katsuo Sueishi
; APPLICANT: Yasuhiro Ikeda
; APPLICANT: Yoshiyuki Inada
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
; FILE REFERENCE: 2733 USOP
; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Human
US-10-276-971-3
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Query Match	100.0%;	Score	228;	DB	15;	Length	228;
Best Local Similarity	100.0%;	Pred. No.	6.4e-66;				
Matches	228;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	CAGCCAGATCAATCAATGCCAGTCCAGTCACTGCTGTATTAACCTTACCATTAGGAATC	60				
Db	1	CAGCCAGATCAATCAATGCCAGTCCAGTCACTGCTGTATTAACCTTACCATTAGGAATC	60				
Qy	61	TCAGTGCAGAGGTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT	120				
Db	61	TCAGTGCAGAGGTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT	120				
Qy	121	GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT	180				
Db	121	GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT	180				

Qy 181 CAGGATTCCATGGACCCTGGACAAGCAAAACCCAAACTCCGAAGACT 228
|||
Db 181 CAGGATTCCATGGACCCTGGACAAGCAAAACCCAAACTCCGAAGACT 228

121	GTGATCTTCAAGACCATTTGTGTGCTGACCCCAAGCAGAAAGTGGGTT	180
Qy		
243	GTGATCTTCAAGACCATTTGTGTGCTGACCCCAAGCAGAAAGTGGGTT	302
Db		
181	CAGGATTCCTATGACCACTCTGGACAGCAAACTCCGAAGACT	228
Qy		
303	CAGGATTCCTATGACCACTCTGGACAGCAAACTCCGAAGACT	350
Db		

RESULT a

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RESULTS
US-10-283-975A-58
; Sequence 58, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods for Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 725
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-58

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Query Match	100.0%; Score 228; DB 17; Length 725;
Best Local Similarity	100.0%; Pred. No. 1e-65;
Matches 228; Conservative	0; Mismatches 0; Indels 0; Gaps 0
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Db	123 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 182
QY	61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCCAAGAAGCT 120
Db	183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCCAAGAAGCT 242
QY	121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGGTGGGTT 180
Db	243 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGGTGGGTT 302
QY	181 CAGGANTTCCATGGACCACTGGCAAGCAACCCAAACTCCGAAGACT 228
Db	303 CAGGANTTCCATGGACCACTGGCAAGCAACCCAAACTCCGAAGACT 350

RESULT 9

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RESULT 9
US-10-764-649-17
; Sequence 17, Application US/10764649
; Publication No. US20040157253A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; APPLICANT: Chen, Hong
; APPLICANT: Barnes, Glenn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE OF
; TITLE OF INVENTION: INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: METABOLIC DISORDERS
; FILE REFERENCE: MPI2003-025P1RM
; CURRENT APPLICATION NUMBER: US/10/764,649
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/446041
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 20

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RESULT 13
US-10-641-643-1165
; Sequence 1165, Application US/10641643
; Publication NO. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641.643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G187434
SEQUENCE DESCRIPTION: SEQ ID NO: 1165 :
US-10-641-643-1165.

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Best Local Similarity 100.0%; Pred. No. 1e-65; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 199 TCAGTGCAGAGGCTCGGAGCTATAGAGAAATCACAGAGCAAGTGTCCCAAGAGACT 258
QY 121 GTGATCTTCAAGACCACTTGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
DB 259 GTGATCTTCAAGACCACTTGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 318
QY 181 CAGGATTCATGCAACCACTTGACAGCAAGCAAAACCCAAATCCGAAGACT 228
DB 319 CAGGATTCATGCAACCACTTGACAGCAAGCAAAACCCAAATCCGAAGACT 366

RESULT 14
US-10-133-013-210
; Sequence 210, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 210
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 470784cB1
US-10-133-013-210

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Best Local Similarity 100.0%; Pred. No. 1e-65; Indels 0; Gaps 0;
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QY 181 CAGGATTCATGCAACCACTTGACAGCAAGCAAAACCCAAATCCGAAGACT 228
DB 322 CAGGATTCATGCAACCACTTGACAGCAAGCAAAACCCAAATCCGAAGACT 369

RESULT 15
US-10-388-360-377
; Sequence 377, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 377
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-377

Query Match 100.0%; Score 228; DB 13; Length 757;
Best Local Similarity 100.0%; Pred. No. 1e-65; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAAATCACAGAGCAAGTGTCCCAAGAGACT 120
DB 201 TCAGTGCAGAGGCTCGGAGCTATAGAGAAATCACAGAGCAAGTGTCCCAAGAGACT 260
QY 121 GTGATCTTCAAGACCACTTGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
DB 261 GTGATCTTCAAGACCACTTGCCAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 320
QY 181 CAGGATTCATGCAACCACTTGACAGCAAGCAAAACCCAAATCCGAAGACT 228
DB 321 CAGGATTCATGCAACCACTTGACAGCAAGCAAAACCCAAATCCGAAGACT 368

Search completed: August 31, 2004, 09:18:28
Job time : 256 secs

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:12 ; Search time 1941 Seconds
(without alignments)
4133.145 Million cell updates/sec

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Perfect score: 228

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Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 145 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	100.0	228	48	US-10-276-971-3
2	228	100.0	294	51	US-10-449-831A-209
3	228	100.0	348	20	US-09-442-384A-161
4	228	100.0	348	20	US-09-442-384B-161
5	228	100.0	349	16	US-09-221-481-519
6	228	100.0	349	20	US-09-442-366A-1139
7	228	100.0	349	20	US-09-442-384-161
8	228	100.0	349	20	US-09-442-589A-37
9	228	100.0	349	20	US-09-442-589B-37
10	228	100.0	392	22	US-09-534-843-7971
11	228	100.0	403	17	US-09-287-618-15642
12	228	100.0	405	51	US-10-449-831A-213
13	228	100.0	425	17	US-09-287-618-16749
14	228	100.0	437	31	US-09-726-791-973
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17	228	100.0	459	33	US-09-823-301-8626
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28	228	100.0	516	31	US-09-721-588-1376
29	228	100.0	520	22	US-09-534-843-7960
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31	228	100.0	522	22	US-09-534-843-7963
32	228	100.0	530	33	US-09-823-301-6829
33	228	100.0	532	22	US-09-534-843-7951
34	228	100.0	545	22	US-09-534-843-7954
35	228	100.0	557	30	US-09-710-286-1702
36	228	100.0	559	27	US-09-652-128-6130
37	228	100.0	565	33	US-09-824-130-501
38	228	100.0	572	22	US-09-534-843-7962
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42	228	100.0	591	22	US-09-534-843-7967
43	228	100.0	647	32	US-09-777-430A-72
44	228	100.0	680	27	US-09-652-128-8614
45	228	100.0	682	29	US-09-699-998-7825

ALIGNMENTS

RESULT 1
 US-10-276-971-3
 ; Sequence 3, Application US/10276971
 ; GENERAL INFORMATION:
 ; APPLICANT: Egashira Kensuke
 ; APPLICANT: Yoshikazu Yonemitsu
 ; APPLICANT: Katsuo Sueishi
 ; APPLICANT: Yasuhiro Ikeda
 ; APPLICANT: Yoshiyuki Inada
 ; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
 ; FILE REFERENCE: 2733 USOP
 ; CURRENT APPLICATION NUMBER: US/10/276,971
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 4
 ; SEQ ID NO 3
 ; LENGTH: 228
 ; TYPE: DNA
 ; ORGANISM: Human

Query Match 100.0%; Score 228; DB 48; Length 228;
 Best Local Similarity 100.0%; Pred. No. 6.9e-58;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 CAGCCAGATCAATCAATGCCCGAGTCACTGCTGTATATACTTACCAATAGGAGATC 60
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RESULT 2

US-10-449-831A-209
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 ; GENERAL INFORMATION:
 ; APPLICANT: Koentgen, Frank
 ; TITLE OF INVENTION: Higher molecular weight entities and uses therefor
 ; FILE REFERENCE: 2385978
 ; CURRENT APPLICATION NUMBER: US/10/449,831A
 ; CURRENT FILING DATE: 2003-05-30
 ; PRIOR APPLICATION NUMBER: USSN 60/384878
 ; PRIOR FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 237
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 209
 ; LENGTH: 294
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: CDS
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 Best Local Similarity 100.0%; Pred. No. 7.5e-58;
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 ; Sequence 161, Application US/09442384A
 ; GENERAL INFORMATION:
 ; APPLICANT: Chencik, Alex
 ; APPLICANT: Lukashchev, Matvey
 ; TITLE OF INVENTION: Hematology/Immunology Array

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; CURRENT APPLICATION NUMBER: US/09/442,384A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384A-161

Query Match      100.0%; Score 228; DB 20; Length 348;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATAACTTCCCAATAGGAAGATC 60
Db      104 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATAACTTCCCAATAGGAAGATC 163

QY      61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db      164 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 223

QY      121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
Db      224 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 283

QY      181 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCCAAGACT 228
Db      284 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCCAAGACT 331

RESULT 4
US-09-442-384B-161
; Sequence 161, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: US/09/442,384B
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384B-161

Query Match      100.0%; Score 228; DB 20; Length 348;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATAACTTCCCAATAGGAAGATC 60
Db      104 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATAACTTCCCAATAGGAAGATC 163

QY      61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db      164 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 223

QY      121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
Db      224 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 283

QY      181 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCCAAGACT 228
Db      284 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCCAAGACT 331

RESULT 5
US-09-221-481-519
; Sequence 519, Application US/09221481
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-008CIP6
; CURRENT APPLICATION NUMBER: US/09/221,481
; CURRENT FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 519
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-221-481-519

Query Match      100.0%; Score 228; DB 16; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATAACTTCCCAATAGGAAGATC 60
Db      104 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATAACTTCCCAATAGGAAGATC 163

QY      61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
Db      164 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 223

QY      121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 180
Db      224 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAAGTGGGTT 283

QY      181 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCCAAGACT 228
Db      284 CAGGATTCATGGACCACTGCGAGCAAGCAACCCAACTCCCAAGACT 331

RESULT 6
US-09-442-366A-1139
; Sequence 1139, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-008CIP13
; CURRENT APPLICATION NUMBER: US/09/442,366A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1139
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-1139

Query Match      100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCCAGATGCAATCAATGCCCGAGTCACTGCTGTATAACTTCCCAATAGGAAGATC 60
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Db 104 CAGCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACTTCCCAATAGGAAGATC 163
Qy 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 331

RESULT 7

US-09-442-384-161
; Sequence 161, Application US/09442384
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384-161

Query Match 100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACTTCCCAATAGGAAGATC 60
Db 104 CAGCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACTTCCCAATAGGAAGATC 163
Qy 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 331

RESULT 8

US-09-442-589A-37
; Sequence 37, Application US/09442589A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Human Cardiovascular Array
; FILE REFERENCE: CLON-006CIP10
; CURRENT APPLICATION NUMBER: US/09/442,589A
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 597
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 37
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleic acid probe
US-09-442-589A-37

Query Match 100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACTTCCCAATAGGAAGATC 60
Db 104 CAGCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACTTCCCAATAGGAAGATC 163
Qy 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 331

RESULT 9

US-09-442-589B-37
; Sequence 37, Application US/09442589B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Human Cardiovascular Array
; FILE REFERENCE: CLON-006CIP10
; CURRENT APPLICATION NUMBER: US/09/442,589B
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1194
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleic acid probe
US-09-442-589B-37

Query Match 100.0%; Score 228; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACTTCCCAATAGGAAGATC 60
Db 104 CAGCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACTTCCCAATAGGAAGATC 163
Qy 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 120
Db 164 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 223
Qy 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 224 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 283
Qy 181 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 228
Db 284 CAGGATTCATGGACCACTGGACAAAGCAAAACCAAACTCCGAAGACT 331

RESULT 10


```
US-09-534-843-7971
; Sequence 7971, Application US/09534843
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLECULE
; FILE REFERENCE: PD-1007 CIP
; CURRENT APPLICATION NUMBER: US/09/534,843
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 49783
; SOFTWARE: PERL Program
; SEQ ID NO 7971
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu01345546
US-09-534-843-7971

Query Match      100.0%; Score 228; DB 22; Length 392;
Best Local Similarity 100.0%; Pred. No. 8.2e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 60
DB      126 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 185

QY      61  TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB      186 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 245

QY      121 GTGATCTTCAAGACCAATTGGCCAGGAGATCTGTCTGACCCCAAGCAGAAAGTGGGTT 180
DB      246 GTGATCTTCAAGACCAATTGGCCAGGAGATCTGTCTGACCCCAAGCAGAAAGTGGGTT 305

QY      181 CAGGATTCATGGACCACTGGACAAAGCAACCCAACTCCGAAGACT 228
DB      306 CAGGATTCATGGACCACTGGACAAAGCAACCCAACTCCGAAGACT 353

RESULT 11
US-09-287-618-15642
; Sequence 15642, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15642
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(403)
; OTHER INFORMATION: n = A,T,C or G
US-09-287-618-15642

Query Match      100.0%; Score 228; DB 17; Length 403;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 60
```

```
DB      118 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 177

QY      61  TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB      178 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 237

QY      121 GTGATCTTCAAGACCAATTGGCCAGGAGATCTGTCTGACCCCAAGCAGAAAGTGGGTT 180
DB      238 GTGATCTTCAAGACCAATTGGCCAGGAGATCTGTCTGACCCCAAGCAGAAAGTGGGTT 297

QY      181 CAGGATTCATGGACCACTGGACAAAGCAACCCAACTCCGAAGACT 228
DB      298 CAGGATTCATGGACCACTGGACAAAGCAACCCAACTCCGAAGACT 345

RESULT 12
US-10-449-831A-213
; Sequence 213, Application US/10449831A
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; TITLE OF INVENTION: Higher molecular weight entities and uses therefor
; FILE REFERENCE: 2385978
; CURRENT APPLICATION NUMBER: US/10/449,831A
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: USSN 60/384878
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 213
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human MCP-1 chimeric construct
; NAME/KEY: CDS
; LOCATION: (1)-(399)
US-10-449-831A-213

Query Match      100.0%; Score 228; DB 51; Length 405;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 60
DB      145 CAGCCAGATGCAATCAATGCCCCAGTCACTGCTGTATTAACCTTCCCAATAGGAAGATC 204

QY      61  TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB      205 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAAGCT 264

QY      121 GTGATCTTCAAGACCAATTGGCCAGGAGATCTGTCTGACCCCAAGCAGAAAGTGGGTT 180
DB      265 GTGATCTTCAAGACCAATTGGCCAGGAGATCTGTCTGACCCCAAGCAGAAAGTGGGTT 324

QY      181 CAGGATTCATGGACCACTGGACAAAGCAACCCAACTCCGAAGACT 228
DB      325 CAGGATTCATGGACCACTGGACAAAGCAACCCAACTCCGAAGACT 372

RESULT 13
US-09-287-618-16749
; Sequence 16749, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSeq for Windows Version 3.0
```

; SEQ ID NO 16749

; LENGTH: 425

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-287-618-16749

Query Match 100.0%; Score 228; DB 17; Length 425;
Best Local Similarity 100.0%; Pred. No. 8.4e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAATC 60
DB 123 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAATC 182
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAAGAGCT 120
DB 183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAAGAGCT 242
QY 121 GTGATCTTCAAGACCATTTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 243 GTGATCTTCAAGACCATTTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 302
QY 181 CAGGATTCATGGACCACTTGGCAAGCAAGCAAACTCCGAAGACT 228
DB 303 CAGGATTCATGGACCACTTGGCAAGCAAGCAAACTCCGAAGACT 350

RESULT 14

US-09-726-791-973

; Sequence 973, Application US/09726791

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Holtzman, Douglas A.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; FILE REFERENCE: THEREFOR

; CURRENT APPLICATION NUMBER: US/09/726,791

; CURRENT FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: 60/168,127

; PRIOR FILING DATE: 1999-11-30

; NUMBER OF SEQ ID NOS: 1870

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 973

; LENGTH: 437

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(437)

; OTHER INFORMATION: n = A,T,C or G

US-09-726-791-973

Query Match 100.0%; Score 228; DB 31; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.5e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAATC 60
DB 132 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAATC 191
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAAGAGCT 120
DB 192 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAAGAGCT 251
QY 121 GTGATCTTCAAGACCATTTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 252 GTGATCTTCAAGACCATTTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 311
QY 181 CAGGATTCATGGACCACTTGGCAAGCAAGCAAACTCCGAAGACT 228
DB 312 CAGGATTCATGGACCACTTGGCAAGCAAGCAAACTCCGAAGACT 359

RESULT 15

US-09-534-843-7953

; Sequence 7953, Application US/09534843

; GENERAL INFORMATION:

; APPLICANT: Seilhamer, Jeffrey J.

; APPLICANT: Deleage, Angelo M.

; APPLICANT: Stuart, Susan G.

; APPLICANT: Stuve, Laura L.

; APPLICANT: Mullaly, Sara J.

; APPLICANT: Naughton, Rebecca E.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLEC

; FILE REFERENCE: PD-1007 CIP

; CURRENT APPLICATION NUMBER: US/09/534,843

; CURRENT FILING DATE: 2000-03-24

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 49783

; SOFTWARE: PERL Program

; SEQ ID NO 7953

; LENGTH: 454

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: hu01000080

US-09-534-843-7953

Query Match 100.0%; Score 228; DB 22; Length 454;
Best Local Similarity 100.0%; Pred. No. 8.6e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAATC 60
DB 123 CAGCCAGATGCAATCAATGCCAGTCCAGTCACTGCTGTATTAACTTCCCAATAGGAATC 182
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAAGAGCT 120
DB 183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAAATCACCAGCAGCAAGTGTCCCAAAGAGCT 242
QY 121 GTGATCTTCAAGACCATTTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 180
DB 243 GTGATCTTCAAGACCATTTGGCCAAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGTT 302
QY 181 CAGGATTCATGGACCACTTGGCAAGCAAGCAAACTCCGAAGACT 228
DB 303 CAGGATTCATGGACCACTTGGCAAGCAAGCAAACTCCGAAGACT 350

Search completed: August 31, 2004, 04:19:46

Job time : 1944 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:12 ; Search time 1465 Seconds
(without alignments)
4647.493 Million cell updates/sec

Title: 07330446

Perfect score: 228

Sequence: 1 cagccagatgcaatcaatgc.....aaacccaactccgaagact 228

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	228	100.0	432	9	AV661469
2	228	100.0	497	9	AA047099
3	228	100.0	513	9	AV714555
4	228	100.0	549	13	EX490080

5	228	100.0	563	12	BM704915
6	228	100.0	588	12	BM708613
7	228	100.0	593	12	BM888255
8	228	100.0	594	13	BQ831442
9	228	100.0	616	9	AL697816
10	228	100.0	623	10	AW772091
11	228	100.0	628	13	BU730951
12	228	100.0	634	13	BQ631169
13	228	100.0	640	12	BM973445
14	228	100.0	640	13	BU85364
15	228	100.0	644	13	BQ573817
16	228	100.0	647	14	CD638814
17	228	100.0	649	14	CB267966
18	228	100.0	652	10	BF339323
19	228	100.0	657	9	AV661137
20	228	100.0	670	14	CD686424
21	228	100.0	673	14	CD638839
22	228	100.0	673	14	CD640282
23	228	100.0	683	10	BF343817
24	228	100.0	691	14	CD641143
25	228	100.0	708	14	CD523445
26	228	100.0	710	14	CD641497
27	228	100.0	713	14	CA440694
28	228	100.0	713	14	CD641186
29	228	100.0	720	14	CD640058
30	228	100.0	723	14	CD522423
31	228	100.0	727	9	AV716926
32	228	100.0	732	12	BQ001668
33	228	100.0	737	14	CA307389
34	228	100.0	738	14	CD641135
35	228	100.0	745	9	AV717442
36	228	100.0	745	13	BU99251
37	228	100.0	751	14	CA448393
38	228	100.0	754	14	CD520218
39	228	100.0	762	9	AV733621
40	228	100.0	766	13	BQ224954
41	228	100.0	787	13	BU192217
42	228	100.0	789	14	CD522574
43	228	100.0	794	13	BQ432639
44	228	100.0	824	13	BU601003
45	228	100.0	852	10	BF211527

ALIGNMENTS

RESULT 1	AV661469	432 bp	mRNA	linear	EST 16-JAN-2002
LOCUS	AV661469	GLC Homo sapiens	CDNA clone	GLCGSG05 3'	mRNA sequence.
DEFINITION	AV661469				
ACCESSION	AV661469.1	GI:9882483			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (Bases 1 to 432)				
AUTHORS	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.				
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	98 (26)			15089-15094 (2001)
MEDLINE	21625106				
PUBMED	11752456				
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919 (ex.45)				

Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source

High quality sequence stop: 487.
Location/Qualifiers
1..497
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3803121"
/db_xref="taxon:9606"
/clone="IMAGE:488534"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares pregnant uterus NbHPU"
/note="Organ: uterus; Vector: pT73-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
ACTGGAAGATTCGGCGCCCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 228; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.1e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCATTAGGAGATC 60
DB 116 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCATTAGGAGATC 175
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 176 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 235
QY 121 GTGATCTTCAGACCAATGTCGCCAGGAGATCTGTGCTGACCCAGCAGCAAGTGGGTT 180
DB 236 GTGATCTTCAGACCAATGTCGCCAGGAGATCTGTGCTGACCCAGCAGCAAGTGGGTT 295
QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 228
DB 296 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 343

RESULT 2

AA047099 497 bp mRNA linear EST 11-MAY-1997
LOCUS 2k74a08.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone
DEFINITION IMAGE:488534.5' similar to gb:M24545 MONOCYTE CHEMOTACTIC PROTEIN 1
PRECUSOR (HUMAN); mRNA sequence.

ACCESSION

AA047099.1 GI:1525016
VERSION EST.

KEYWORDS

Source Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)

REFERENCE

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., DuBuque, T., Favell, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
and Marra, M.

TITLE

Generation and analysis of 280,000 human expressed sequence tags

JOURNAL

Genome Res. 6 (9), 807-828 (1996)

MEDLINE

97044478

PUBMED

8889549

COMMENT

Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
This clone is available royalty-free through INLNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 741 Std Error: 0.00
Seq primer: -28M3 rev2 from Amersham

FEATURES

source

This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..513
/organism="Homo sapiens"

ORIGIN

Query Match 100.0%; Score 228; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCATTAGGAGATC 60
DB 70 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCATTAGGAGATC 129
QY 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 120
DB 130 TCAGTGCAGAGGCTCGCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAGAAGCT 189
QY 121 GTGATCTTCAGACCAATGTCGCCAGGAGATCTGTGCTGACCCAGCAGCAAGTGGGTT 180
DB 190 GTGATCTTCAGACCAATGTCGCCAGGAGATCTGTGCTGACCCAGCAGCAAGTGGGTT 249
QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 228
DB 250 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAGACT 297

RESULT 3

AV714555 513 bp mRNA linear EST 11-OCT-2000
LOCUS AV714555 DCB Homo sapiens cDNA clone DCBADG05.5', mRNA sequence.
DEFINITION AV714555
ACCESSION AV714555
VERSION AV714555.1 GI:10796072
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 513)

REFERENCE

AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,
Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,
Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Cheng, Z., and Han, Z.

TITLE

Homo sapiens cDNA DCB clones

JOURNAL

Unpublished (2000)

COMMENT

Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn

Query Match 100.0%; Score 228; DB 13; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 60
DB 138 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 197
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 198 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 257
QY 121 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 258 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 317
QY 181 CAGGATTCATGAGCACCCTGGACAGCAAGCAAACTCCGAGAGCT 228
DB 318 CAGGATTCATGAGCACCCTGGACAGCAAGCAAACTCCGAGAGCT 365
RESULT 5
BM704915 563 bp mRNA linear EST 28-FEB-2002
LOCUS UI-E-CII-agf-h-04-0-UI.r1 UI-E-CII Homo sapiens cDNA clone
DEFINITION UI-E-CII-agf-h-04-0-UI 5', mRNA sequence.
ACCESSION BM704915
VERSION BM704915.1 GI:19018173
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 563)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bent-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1..563
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CII-agf-h-04-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pRT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CII is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBADG05"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_lib="DCB"
/note="Vector: pTriplex2; Site_1: sfIIA; Site_2: sfIIB"
ORIGIN
Query Match 100.0%; Score 228; DB 9; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 60
DB 134 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATTAATTCACCAATAGGAAGATC 193
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 120
DB 194 TCAGTGCAGAGGCTCGGAGCTATAGAGATCACCAGCAGCAAGTGTCCCAAGAGCT 253
QY 121 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
DB 254 GTGATCTTCAAGACCACTTGTGGCCAAAGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 313
QY 181 CAGGATTCATGAGCACCCTGGACAGCAAGCAAACTCCGAGAGCT 228
DB 314 CAGGATTCATGAGCACCCTGGACAGCAAGCAAACTCCGAGAGCT 361
RESULT 4
BX490080 549 bp mRNA linear EST 04-SEP-2003
LOCUS DKFP686B1371_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFP686B1371 5', mRNA sequence.
ACCESSION BX490080
VERSION BX490080.1 GI:31999304
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 549)
AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaun,S., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and Wiemann,S.
TITLE EST (Ottenwaelder,B., Obermaier,B., Deutschenbaun,S., Mewes,H.W., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available.
This clone (DKFP686B1371) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686B1371"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: sfIIA; Site_2: sfIIB; cDNA-collection"
ORIGIN

adaptor, digested with Not I, and cloned directionally into pTV73 vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)_n tail. The sequence tag for this library is ACCGAC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NIH).

ORIGIN

Query Match	100.0%	Score 228;	DB 12;	Length 563;
Best Local Similarity	100.0%;	Pred. No. 1.3e-52;		
Matches 228;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCAGTGGAGATC	60	
Db	108	CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTATTAACCTCACCAGTGGAGATC	167	
QY	61	TCAGTGCAGAGGCTCGCGAGCTTAGAGAATCACCAGCAGCAAGTGTCCCAAGAAAGCT	120	
Db	168	TCAGTGCAGAGGCTCGCGAGCTTAGAGAATCACCAGCAGCAAGTGTCCCAAGAAAGCT	227	
QY	121	GTGATCTTCAGACCATTTGGCGCCAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT	180	
Db	228	GTGATCTTCAGACCATTTGGCGCCAGGAGATCTGTGCTGACCCCAAGCAGCAAGTGGGTT	287	
QY	181	CAGGATTCATGGACCACTGGACAAGCAAAACCCAAACTCCGAAGACT	228	
Db	288	CAGGATTCATGGACCACTGGACAAGCAAAACCCAAACTCCGAAGACT	335	

RESULT 6
BM708613
LOCUS BM708613 588 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-C11-afw-i-08-0-UI.r1 UI-E-C11 Homo sapiens cDNA clone
UI-E-C11-afw-i-08-0-UI 5'. mRNA sequence.

BM708513.1	GI:19021871
EST.	
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 588)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBLISHED	8889548
COMMENT	Contact: Soares VB

Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

```

source
1..588
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-R-C11-aiw-i-08-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"

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ORIGIN

Query Match	100.0%;	Score 228;	DB 12;	Length 588;
Best Local Similarity	100.0%;	Pred. No. 1.3e-52;		
Matches 228;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CAGCCAGATCAATCAATGCCCCAGTCACCTGCTGTTATTAACCTCCACCAATAGGAAGATC	60	
Db	108	CAGCCAGATCAATCAATGCCCCAGTCACCTGCTGTTATTAACCTCCACCAATAGGAAGATC	167	
QY	61	TCAGTGCAGAGGCTCGCGAGCTATAGAGAAATCAACAGCAGCAAGTGTGCCAAAGAGCT	120	
Db	168	TCAGTGCAGAGGCTCGCGAGCTATAGAGAAATCAACAGCAGCAAGTGTGCCAAAGAGCT	227	
QY	121	GTGATCTTCAAGACCACTTGTGGCCAGGAGATCTGTGCTGACCCCAACAGCAAGTGGGTT	180	
Db	228	GTGATCTTCAAGACCACTTGTGGCCAGGAGATCTGTGCTGACCCCAACAGCAAGTGGGTT	287	
QY	181	CAGGATTCATGACCACTCGACCAAGCAAAACCCAAATCCCGAAGACT	228	
Db	288	CAGGATTCATGACCACTCGACCAAGCAAAACCCAAATCCCGAAGACT	335	

RESULT 7	ACCESSION	ORGANISM
BM888255	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	

REFERENCE
Zamalya, J.C., Metcalz, A., Wirtz, M.K., Samples, J.R., Xu, H., Severson, T. and Acott, T.S. 1999, Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 593)

AUTHORS
Wirtz, M.K., Samples, J.R., Xu, H., Severson, T. and Acott, T.S.

TITLE
Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library

JOURNAL
Unpublished (2002)

Glaucoma Genetics Lab
 Oregon Health Sciences University
 3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
 Tel: 503-494-4698
 Fax: 503-494-6875
 Email: wirtzm@chu.edu
 Seq primer: T7 Reverse.
 Location/Qualifiers
 1. 593
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="eye"
 /cell_type="trabecular meshwork"
 source:

/lab host="TOP10P."
/clone lib="Human Trabecular Meshwork cDNA library"
/note=vector: pcDNA3; Site 1: EcoRI; Site 2: EcoRI; Human
cDNA library made from mRNA isolated from trabecular
meshwork cells established from eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
and TP010P, host cells."

ORIGIN
Query Match 100.0%; Score 228; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCCTGCTTTATTAACCTTCAACCAATAGGAAGATC 60
DB 124 CAGCCAGATGCAATCAATGCCCCAGTCCCTGCTTTATTAACCTTCAACCAATAGGAAGATC 183
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGATGTCTCCCAAGAGCT 120
DB 184 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGATGTCTCCCAAGAGCT 243
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAAGATGTGGTT 180
DB 244 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAAGATGTGGTT 303
QY 181 CAGGATTCATGACCACTGGACCAAGCAACCCAAATCCGAAGCT 228
DB 304 CAGGATTCATGACCACTGGACCAAGCAACCCAAATCCGAAGCT 351

RESULT 8
BQ631442 594 bp mRNA linear EST 02-JUL-2002
LOCUS il17e04.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6030414 5'
DEFINITION similar to SM:SY02 HUMAN P33500 SMALL INDUCIBLE CYTOKINE A2
PRECUSOR ;, mRNA sequence.

ACCESSION BQ631442.1 GI:21682960
VERSION BQ631442.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 594)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: il17e04.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 48S.
Location/Qualifiers
1..594
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

/db_xref="taxon:9606"
/clone="IMAGE:6030414"
/issue_type="Purified pancreatic islet"
/lab host="DH10B"
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 100.0%; Score 228; DB 13; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCCAGTCCCTGCTTTATTAACCTTCAACCAATAGGAAGATC 60
DB 120 CAGCCAGATGCAATCAATGCCCCAGTCCCTGCTTTATTAACCTTCAACCAATAGGAAGATC 179
QY 61 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGATGTCTCCCAAGAGCT 120
DB 180 TCAGTGCAGAGGCTCGGAGCTATAGAGAATCACCAGCAGATGTCTCCCAAGAGCT 239
QY 121 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAAGATGTGGTT 180
DB 240 GTGATCTTCAAGACCATTTGTGCCAAGAGATCTGTGCTGACCCCAAGCAAGATGTGGTT 299
QY 181 CAGGATTCATGACCACTGGACCAAGCAACCCAAATCCGAAGCT 228
DB 300 CAGGATTCATGACCACTGGACCAAGCAACCCAAATCCGAAGCT 347

RESULT 9
AL697816 616 bp mRNA linear EST 04-SEP-2003
LOCUS DXFZP686E04104.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DXFZP686E04104.5', mRNA sequence.

ACCESSION AL697816
VERSION AL697816.1 GI:19618356
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 616)
Ottewaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
Wiemann, S.
EST (Ottewaelder, B., Obermaier, B., Mewes, H.W., Weil, B. and
Wiemann, S.)

TITLE Unpublished (2001)
JOURNAL Contact: MIPS
COMMENT MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.

This clone (DKFZP686E04104) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
1..616
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686E04104"

FEATURES
source

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/dev stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlc3)"
/notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
CDNA-collection"

ORIGIN
Query Match 100.0%; Score 228; DB 9; Length 616;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATCAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCCACCAATAGGAGATC 60
Db 134 CAGCCAGATCAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCCACCAATAGGAGATC 193
QY 61 TCAGTCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGCT 120
Db 194 TCAGTCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGCT 253
QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 254 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 313
QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAAGACT 228
Db 314 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAAGACT 361

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RESULT 10
AW772091/c
LOCUS
DEFINITION
h67208.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3032942 3'
similar to gb:M24545 MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION
AW772091
VERSION
AW772091.1 GI:7704153
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 623)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
Location/Qualifiers
1. 623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3032942"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/notes="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid1 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs

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FEATURES
source

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(cloneIds 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo.

ORIGIN
Query Match 100.0%; Score 228; DB 10; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATCAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCCACCAATAGGAGATC 60
Db 603 CAGCCAGATCAATCAATGCCCCAGTCACCTGCTGTATTAACCTTCCACCAATAGGAGATC 544
QY 61 TCAGTCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 120
Db 543 TCAGTCAGAGGCTCGCGAGCTATAGAGAATCACCAGCAGCAAGTGTCCCAAGAGACT 484
QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
Db 483 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 424
QY 181 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAAGACT 228
Db 423 CAGGATTCATGACCACTGGACAGCAAAACCCAACTCCGAAGACT 376

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RESULT 11
BU730951/c
LOCUS
DEFINITION
UI-E-C11-afw-i-08-0-UI.s1 UI-E-C11 Homo sapiens cDNA clone
UI-E-C11-afw-i-08-0-UI 3', mRNA sequence.
ACCESSION
BU730951
VERSION
BU730951.1 GI:23655357
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 628)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-33, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. 628
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-C11-afw-i-08-0-UI"
/tissue_type="RPE and Choroid"
/dev stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phase resistant)"
/clone_lib="UIT-P-C11"

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FEATURES
source

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modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-CII is a normalized cDNA library containing the
 following tissue(s): RPE and Choroid. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pRTT3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is ACCATA.
 This library was created for the program, Gene Discovery
 in the Visual System, supported by National Eye Institute
 (NEI).
 TAG TISSUE=RPE and Choroid
 TAG LIB=UI-E-CII
 TAG_SEQ=ACCTA"

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 628;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTACCTGCTGTATTAATTCACCAATAGGAGATC 60
 Db 622 CAGCCAGATGCAATCAATGCCCGAGTACCTGCTGTATTAATTCACCAATAGGAGATC 563

QY 61 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAGCT 120
 Db 562 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAGCT 503

QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 180
 Db 502 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 443

QY 181 CAGGATTCATGACCACTGACAGCAACCAACTCCGAAGCT 228
 Db 442 CAGGATTCATGACCACTGACAGCAACCAACTCCGAAGCT 395

RESULT 12
 BQ631169/c
 LOCUS
 DEFINITION
 similar to SW:SY02 HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2
 PRECURSOR ; mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Q631169.1 GI:21682687
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 634)

REFERENCE
 AUTHORS
 Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Pearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biochem.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center for information on

obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 439.
 Location/Qualifiers
 1..634
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6030414"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
 /notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
 NotI; Site_2: XhoI; cDNA made by oligo-dT priming. ~1kb. 5'
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2892."

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 634;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTACCTGCTGTATTAATTCACCAATAGGAGATC 60
 Db 607 CAGCCAGATGCAATCAATGCCCGAGTACCTGCTGTATTAATTCACCAATAGGAGATC 548

QY 61 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAGCT 120
 Db 547 TCAGTGCAGAGCTCGGAGCTATAGAGATCACAGCAGCAAGTGTCCCAAGAAGCT 488

QY 121 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 180
 Db 487 GTGATCTTCAAGACCATTTGGCCCAAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 428

QY 181 CAGGATTCATGACCACTGACAGCAACCAACTCCGAAGCT 228
 Db 427 CAGGATTCATGACCACTGACAGCAACCAACTCCGAAGCT 380

RESULT 13
 BQ973445/c
 LOCUS
 DEFINITION
 UI-CF-EC1-abx-n-09-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
 UI-CF-EC1-abx-n-09-0-UI 3', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BQ973445.1 GI:19591036
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 640)

REFERENCE
 AUTHORS
 TITLE

Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL
 MEDLINE
 PUBMED

COMMENT

Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-36, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA-Yes.

FEATURES

Location/Qualifiers
 source

1..640
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EC1-abx-n-09-0-UI"
 /tissue_type="lung"
 /dev_stage="Adult and Fetal"
 /lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EC1"
 /notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-EC1 is a normalized cDNA library containing the
 following tissue(s): Normal lung from adult and from fetal
 day 64, day 87, week 19 and week 42. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 AAGTGGCTTAC.
 TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
 and 380-383
 TAG_LIB=UI-CF-EC1
 TAG_SEQ=AAGTGGCTTAC

ORIGIN

Query Match 100.0%; Score 228; DB 12; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAGAGATC 60
 Db 619 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAGAGATC 560
 QY 61 TCAGTCACAGGCTCCGAGCTATAGAAATCACAGCAGCAAGTGTCCCAAGAGCT 120
 Db 559 TCAGTCACAGGCTCCGAGCTATAGAAATCACAGCAGCAAGTGTCCCAAGAGCT 500
 QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 180
 Db 499 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 440
 QY 181 CAGGATTCATGGACCACTGACAGCAAGCAACCCAACTCCGAGACT 228
 Db 439 CAGGATTCATGGACCACTGACAGCAAGCAACCCAACTCCGAGACT 392

RESULT 14

BU685364/c
 LOCUS
 DEFINITION UI-CF-DUI-aav-j-23-0-UI-s2 UI-CF-DUI Homo sapiens cDNA clone
 BU685364
 BU685364.1 GI:23539236
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 640)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-35, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA-Yes.

FEATURES

Location/Qualifiers
 source

1..640
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-DUI-aav-j-23-0-UI"
 /tissue_type="Primary Lung Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-DUI"
 /notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-DUI is a normalized cDNA library containing the
 following tissue(s): Primary Lung Epithelial Cells. The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT7T3-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GGCTGTAGGC.
 TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_LIB=UI-CF-DUI
 TAG_SEQ=GGCTGTAGGC

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAGAGATC 60
 Db 618 CAGCCAGATGCAATCAATGCCAGTCACCTGCTGTATTAACCTCACCAGAGATC 559
 QY 61 TCAGTCACAGGCTCCGAGCTATAGAAATCACAGCAGCAAGTGTCCCAAGAGCT 120
 Db 558 TCAGTCACAGGCTCCGAGCTATAGAAATCACAGCAGCAAGTGTCCCAAGAGCT 499
 QY 121 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 180
 Db 498 GTGATCTTCAAGACCATTTGGCCAGGAGATCTGTGTGACCCCAAGCAAGTGGGTT 439
 QY 181 CAGGATTCATGGACCACTGACAGCAAGCAACCCAACTCCGAGACT 228
 Db 438 CAGGATTCATGGACCACTGACAGCAAGCAACCCAACTCCGAGACT 391

RESULT 15

BQ573817/c
 LOCUS BQ573817.1 644 bp mRNA linear EST 19-JUN-2002
 DEFINITION UI-H-EZO-bax-c-19-0-UI.s1 NCI CGAP Ch1 Homo sapiens CDNA clone
 UI-H-EZO-bax-c-19-0-UI 3', mRNA sequence.
 ACCESSION BQ573817
 VERSION BQ573817
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 644)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
 Orthopaedics

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-39, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers

1..644
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-EZO-bax-c-19-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI-CGAP Ch1"
 /note="Organ: Left Pelvis; Vector: pTT73-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP Ch1 is a cDNA library containing the following
 tissue(s): Chondrosarcoma Grade II. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pTT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (gr)18 tail. The sequence tag for this library is
 TGATCAGCT.
 TAG_TISSUE=grade-2-chondrosarcoma
 TAG_LIB=UI-H-EZO
 TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 100.0%; Score 228; DB 13; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.3e-52;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTTATACTTACCAATAGGAATC 60
 DB 622 CAGCCAGATGCAATCAATGCCCGAGTCACCTGCTGTTATACTTACCAATAGGAATC 563
 QY 61 TCAGTCAGAGGCTCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAAGGCT 120
 DB 562 TCAGTCAGAGGCTCGAGCTATAGAAGATCACCAGCAGCAAGTGTCCCAAAGGCT 503

QY 121 GTGATCTTCAAGACCATTTGCGCCAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGTT 180
 DB 502 GTGATCTTCAAGACCATTTGCGCCAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGTT 443
 QY 181 CAGGATTCCATGGACCAACCTGGACAAAGCAAAACCCAAACTCCGAAGACT 228
 DB 442 CAGGATTCCATGGACCAACCTGGACAAAGCAAAACCCAAACTCCGAAGACT 395

Search completed: August 31, 2004, 03:47:21
 Job time : 1473 secs

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